G.	ag ga In As	c go	t gt .a Va	a go al Al	t to a Se	a aa r Ly	a at s Il	c tt	a gg eu Gl	y Le	g co eu Pr	t ac	g ca ir Gl	ng ac n Th	t gtt ir Val	49
1 gat Asp	tca Ser	tca Ser	cag Gln 20	ggt Gly	tct Ser	gaa Glu	tat Tyr	gac Asp 25	tat	gtc	ata Ile	ttc Phe	aca Thr 30	caa	act	97
act Thr	gaa Glu	aca Thr 35	qca	cac His	tct Ser	tgt Cys	aat Asn 40	gtc	aac Asn	cgc Arg	ttc Phe	aat Asn 45	gtg Val	gct Ala	atc Ile	145
aca Thr	agg Arg 50	qca	aaa Lys	att Ile	ggc Gly	att Ile 55	ttg	tgc Cys	ata Ile	atg Met	tct Ser 60	gat Asp	aga Arg	gat Asp	ctt Leu	193
tat Tyr 65	gac Asp	aaa Lys	ctg Leu	caa Gln	ttt Phe 70	aca Thr	agt Ser	cta Leu	gaa Glu	ata Ile 75	cca Pro	cgt Arg	cgc Arg	aat Asn	gtg Val 80	241
act	aca Thr	tta Leu	caa Gln	gca Ala 85	gaa Glu	aat Asn	gta Val	act Thr	gga Gly 90	ctt Leu	ttt Phe	aag Lys	gac Asp	tgt Cys 95	agt Ser	289
aag Lys	atc Ile	att Ile	act Thr 100	ggt Gly	ctt Leu	cat His	cct Pro	aca Thr 105	cag Gln	gca Ala	cct Pro	aca Thr	cac His 110	ctc Leu	agc Ser	337
gtt Val	gat Asp	ata Ile 115	aaa Lys	ttc Phe	aag Lys	act Thr	gaa Glu 120	gga Gly	tta Leu	tgt Cys	gtt Val	gac Asp 125	ata Ile	cca Pro	ggc Gly	385
Ile	cca Pro 130	Lys	Asp	Met	Thr	Tyr 135	Arg	Arg	Leu	Ile	Ser 140	Met	Met	Gly	Phe	433
Lys 145	atg Met	Asn	Tyr	Gln	Val 150	Asn	Gly	Tyr	Pro	Asn 155	Met	Phe	Ile	Thr	Arg 160	481
Glu	gaa Glu	Ala	Ile	Arg 165	His	Val	Arg	Ala	Trp 170	Ile	Gly	Phe	Asp	Val 175	Glu	529
Ğİy	tgt Cys	His	Ala 180	Thr	Arg	Asp	Ala	Val 185	Gly	Thr	Asn	Leu	Pro 190	Leu	Gln	577
cta Leu	gga Gly	ttt Phe 195	tct Ser	aca Thr	ggt Gly	gtt Val	aac Asn 200	tta Leu	gta Val	gct Ala	gta Val	ccg Pro 205	act Thr	ggt Gly	tat Tyr	625
	gac Asp	Thr														646

FIG. 1

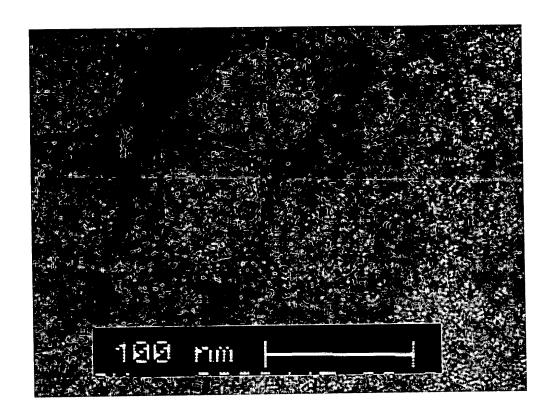


FIG. 2



FIG. 3

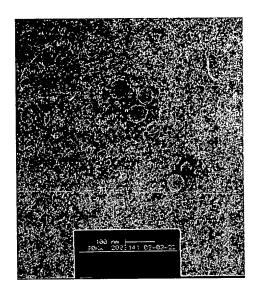


FIG. 4

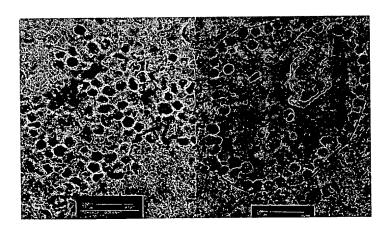


FIG. 5A

FIG. 5B

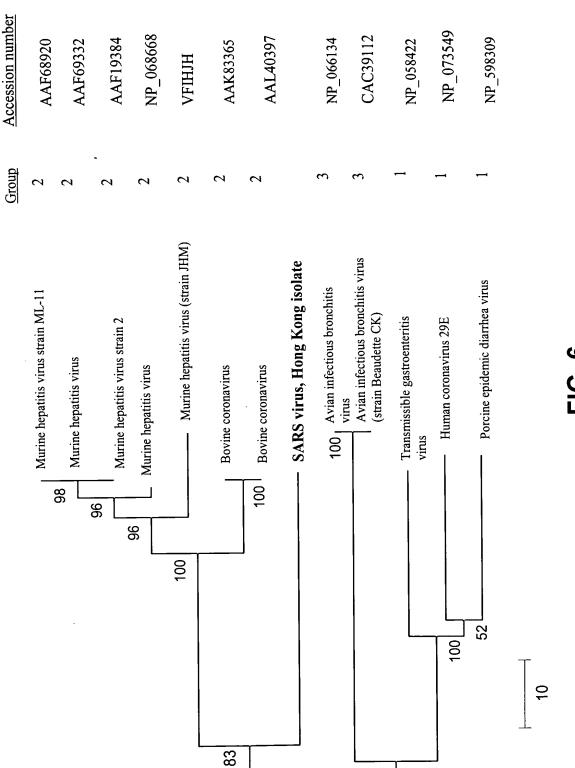


FIG. 6

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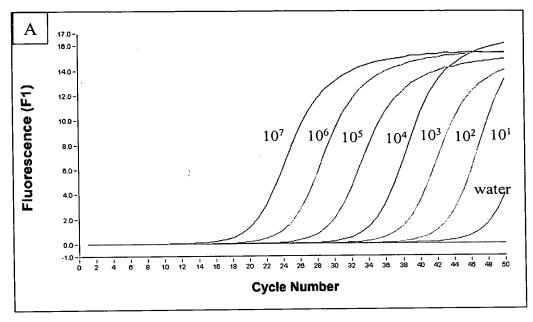


FIG. 7A

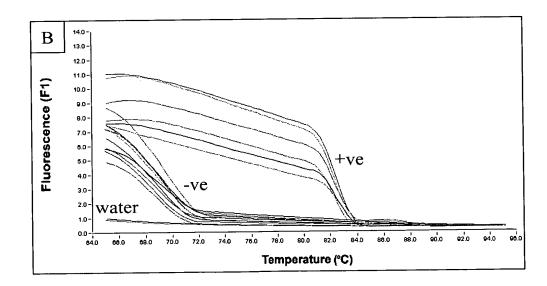


FIG. 7B

t aa Ly 1	a tg s Cy	t ag s Se	t ag r Ar	a at g Il 5	c at e Il	a cc e Pr	t go o Al	g cg a Ar	t gc g Al 10	a Ar	c gt g Va	a ga 1 G1	g tg u Cy	t tt s Ph 15	t gat e Asp	49
aaa Lys	ttc Phe	aaa Lys	gtg Val 20	aat Asn	tca Ser	aca Thr	cta Leu	gaa Glu 25	cag Gln	tat Tyr	gtt Val	ttc Phe	tgc Cys 30	act Thr	gta Val	97 [°]
aat Asn	gca Ala	ttg Leu 35	cca Pro	gaa Glu	aca Thr	act Thr	gct Ala 40	gac Asp	att Ile	gta Val	gtc Val	ttt Phe 45	gat Asp	gaa Glu	atc Ile	145
Ser	atg Met 50	gct Ala	act Thr	aat Asn	tat Tyr	gac Asp 55	ttg Leu	agt Ser	gtt Val	gtc Val	aat Asn 60	gct Ala	aga Arg	ctt Leu	cgt Arg	193
gca Ala 65	aaa Lys	cac His	tac Tyr	gtc Val	tat Tyr 70	att Ile	ggc Gly	gat Asp	cct Pro	gct Ala 75	caa Gln	tta Leu	cca Pro	gcc Ala	ccc Pro 80	241
cgc Arg	aca Thr	ttg Leu	ctg Leu	act Thr 85	aaa Lys	ggc Gly	aca Thr	cta Leu	gaa Glu 90	cca Pro	gaa Glu	tat Tyr	ttt Phe	aat Asn 95	tca Ser	289
gtg Val	tgc Cys	aga Arg	ctt Leu 100	atg Met	aaa Lys	aca Thr	ata Ile	ggt Gly 105	cca Pro	gac Asp	atg Met	ttc Phe	ctt Leu 110	gga Gly	act Thr	337
tgt Cys	cgc Arg	cgt Arg 115	tgt Cys	cct Pro	gct Ala	gaa Glu	att Ile 120	gtt Val	gac Asp	act Thr	gtg Val	agt Ser 125	gct Ala	tta Leu	gtt Val	385
tat Tyr	gac Asp 130	aat Asn	aag Lys	cta Leu	aaa Lys	gca Ala 135	cac His	aag Lys	gag Glu	aag Lys	tca Ser 140	gct Ala	caa Gln	tgc Cys	ttc Phe	433
Lys 145	Met	Phe	Tyr	Lys	ggt Gly 150	Val	Ile	Thr	His	Asp 155	Val	Ser	Ser	Ala	11e 160	481
aac Asn	aga Arg	cct Pro	caa Gln	ata Ile 165	ggc Gly	gtt Val	gta Val	aga Arg	gaa Glu 170	ttt Phe	ctt Leu	aca Thr	cgc Arg	aat Asn 175	cct Pro	529
gct Ala	tgg Trp	aga Arg	aaa Lys 180	gct	gtt Val	ttt Phe	atc Ile	tca Ser 185	cct Pro	tat Tyr	aat Asn	tca Ser	cag Gln 190	aac Asn	gct Ala	577
gta Val	gct Ala	tca Ser 195	aaa Lys	atc Ile	tta Leu	gga Gly	ttg Leu 200	Pro	acg Thr	cag Gln	act Thr	gtt Val 205	Asp	tca Ser	tca Ser	625
cag Gln	ggt Gly 210	Ser	gaa Glu	tat Tyr	gac Asp	tat Tyr 215	Val	ata Ile	ttc Phe	aca Thr	caa Gln 220	Thr	act Thr	gaa Glu	aca Thr	673

gca Ala 225	cac His	tct Ser	tgt Cys	aat Asn	gtc Val 230	aac Asn	cgc Arg	ttc Phe	aat Asn	gtg Val 235	gct Ala	atc Ile	aca Thr	agg Arg	gca Ala 240	721
aaa Lys	att Ile	ggc Gly	att Ile	ttg Leu 245	tgc Cys	ata Ile	atg Met	tct Ser	gat Asp 250	aga Arg	gat Asp	ctt Leu	tat Tyr	gac Asp 255	aaa Lys	769
ctg Leu	caa Gln	ttt Phe	aca Thr 260	agt Ser	cta Leu	gaa Glu	ata Ile	cca Pro 265	cgt Arg	cgc Arg	aat Asn	gtg Val	gct Ala 270	aca Thr	tta Leu	817
caa Gln	gca Ala	gaa Glu 275	aat Asn	gta Val	act Thr	gga Gly	ctt Leu 280	ttt Phe	aag Lys	gac Asp	tgt Cys	agt Ser 285	aag Lys	atc Ile	att Ile	865
act Thr	ggt Gly 290	ctt Leu	cat His	cct Pro	aca Thr	cag Gln 295	gca Ala	cct Pro	aca Thr	cac His	ctc Leu 300	agc Ser	gtt Val	gat Asp	ata Ile	913
aaa Lys 305	ttc Phe	aag Lys	act Thr	gaa Glu	gga Gly 310	tta Leu	tgt Cys	gtt Val	gac Asp	ata Ile 315	cca Pro	ggc Gly	ata Ile	cca Pro	aag Lys 320	961
gac Asp	atg Met	acc Thr	tac Tyr	cgt Arg 325	aga Arg	ctc Leu	atc Ile	tct Ser	atg Met 330	Met	ggt Gly	ttc Phe	aaa Lys	atg Met 335	aat Asn	1009
tac Tyr	caa Gln	gtc Val	aat Asn 340	ggt Gly	tac Tyr	cct Pro	aat Asn	atg Met 345	ttt Phe	atc Ile	acc Thr	cgc Arg	gaa Glu 350	gaa Glu	gct Ala	1057
att Ile	cgt Arg	cac His 355	gtt Val	cgt Arg	gcg Ala	tgg Trp	att Ile 360	Gly	ttt Phe	gat Asp	gta Val	gag Glu 365	Gly	tgt Cys	cat His	1105
gca Ala	act Thr 370	Arg	gat Asp	gct Ala	gtg Val	ggt Gly 375	Thr	aac Asn	cta Leu	cct Pro	ctc Leu 380	GIn	cta Leu	gga Gly	ttt Phe	1153
tct Ser 385	Thr	ggt Gly	gtt Val	aac Asn	tta Leu 390	Val	gct Ala	gta Val	ccg Pro	act Thr 395	ggt Gly	tat Tyr	gtt Val	gac Asp	act Thr 400	1201
gaa	aat	aac	cta	L			Glu	Asn	Asn	Leu						1213

FIG. 8 Con't

c ag Ar 1	a ac g Th	c at r Me	g cc t Pr	t aa o As 5	ic at sn Me	g ct t Le	t ag u Ar	g at g Il	a at e Me	t Al	cc to la Se	t ct r Le	t gt u Va	t ct l Le	t gct u Ala	49
cgc Arg	aaa Lys	cat His	aac Asn 20	act Thr	tgc Cys	tgt Cys	aac Asn	tta Leu 25	tca Ser	cac His	cgt Arg	ttc Phe	tac Tyr 30	agg Arg	tta Leu	97
gct Ala	aac Asn	gag Glu 35	tgt Cys	gcg Ala	caa Gln	gta Val	tta Leu 40	agt Ser	gag Glu	atg Met	gtc Val	atg Met 45	tgt Cys	ggc Gly	ggc Gly	145
tca Ser	cta Leu 50	tat Tyr	gtt Val	aaa Lys	cca Pro	ggt Gly 55	gga Gly	aca Thr	tca Ser	tcc Ser	ggt Gly 60	gat Asp	gct Ala	aca Thr	act Thr	193
gct Ala 65	tat Tyr	gct Ala	aat Asn	agt Ser	gtc Val 70	ttt Phe	aac Asn	att Ile	tgt Cys	caa Gln 75	gct Ala	gtt Val	aca Thr	gcc Ala	aat Asn 80	241
gta Val	aat Asn	gca Ala	ctt Leu	ctt Leu 85	tca Ser	act Thr	gat Asp	ggt Gly	aat Asn 90	aag Lys	ata Ile	gct Ala	gac Asp	aag Lys 95	tat Tyr	289
gtc Val	cgc Arg	aat Asn	cta Leu 100	caa Gln	cac His	agg Arg	ctc Leu	tat Tyr 105	gag Glu	tgt Cys	ctc Leu	tat Tyr	aga Arg 110	aat Asn	agg Arg	337
gat Asp	gtt Val	gat Asp 115	cat His	gaa Glu	ttc Phe	gtg Val	gat Asp 120	gag Glu	ttt Phe	tac Tyr	gct Ala	tac Tyr 125	ctg Leu	cgt Arg	aaa Lys	385
cat His	ttc Phe 130	tcc Ser	atg Met	atg Met	att Ile	ctt Leu 135	tct Ser	gat Asp	gat Asp	gcc Ala	gtt Val 140	gtg Val	tgc Cys	tat Tyr	aac Asn	433
Ser 145	Asn	Tyr	Ala	Ala	Gln 150	Gly	Leu	Val	Ala	Ser 155		Lys	Asn	Phe	Lys 160	481
gca Ala	gtt Val	ctt Leu	tat Tyr	tat Tyr 165	caa Gln	aat Asn	aat Asn	gtg Val	ttc Phe 170	atg Met	tct Ser	Glu	gca Ala S	aaa Lys 175	tgt Cys	529
Trp	Thr	Glu	Thr 180	Asp	Leu	Thr	Lys	Gly 185	Pro	His	gaa Glu	Phe	Cys 190	Ser	Gln	577
His	Thr	Met 195	Leu	Val	Lys	Gln	Gly 200	Asp	Asp	Tyr	· Val	Tyr 205	Leu	Pro		625
Pro	Asp 210	Pro	Ser	Arg	Ile	Leu 215	Gly	Ala	Gly	Cys	ttt Phe 220	Val	Asp	Asp	Ile	673
gtc Val 225	Lys	cag Gln	atg Met	gta Val	cac His 230	tta Leu	tga	ttg	aaa	ggt	tcc	gtg	tca	ctg	gct	721
2++	an t	~~														729

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121	gcagtataaa	caataataaa	ttttactgtc	gttgacaaga	aacgagtaac	tcgtccctct
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481	cqttctgatg	ccttaagcac	caatcacggc	cacaaggtcg	ttgagctggt	tgcagaaatg
541	gacggcattc	agtacggtcg	tagcggtata	acactgggag	tactcgtgcc	acatgtgggc
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1081	tttgtgtttc	ctcttaactc	aaaagtcaaa	gtcattcaac	cacgtgttga	aaagaaaaag
1141	actgagggtt	tcatggggcg	tatacgctct	gtgtaccctg	ttgcatctcc	acaggagtgt
1201	aacaatatgc	acttgtctac	cttgatgaaa	tgtaatcatt	gcgatgaagt	ttcatggcag
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1441	attgaaactc	gactccgcaa	gggaggtagg	actagatgtt	ttggaggctg	tgtgtttgcc
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1561	tcaggccata	ctggcattac	tggtgacaat	gtggagacct	tgaatgagga	tctccttgag
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1981	atttctgaac	agtcattacg	tcttgtcgac	gccatggttt	atacttcaga	cctgctcacc
2041	aacagtgtca	ttattatggc	atatgtaact	ggtggtcttg	tacaacagac	tteteagtgg
2101	ttgtctaatc	ttttgggcac	tactgttgaa	aaactcaggc	ctatctttga	acggactgag
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2221	attacaggtg	tttttgacat	cgtcaagggt	caaatacagg	tegetteaga	cattactaag
2281	gattgtgtaa	aatgcttcat	tgatgttgtt	aacaaggcac	ccgaaatgtg	cattgattaa
2341	gtcactatcg	ctggcgcaaa	gttgcgatca	ctcaacttag	grgaagreer	actogeteaa
2401	agcaagggac	tttaccgtca	gtgtatacgt	ggcaaggagc	agetgeaact	actuatgue
2461	cttaaggcac	caaaagaagt	aacctttctt	gaaggtgatt	tagagagag	agtacttact
2521	tctgaggagg	ttgttctcaa	gaacggtgaa	ctegaageae	ataggatgat	agtattaga
2581	ttcacaaatg	gagetategt	cggcacacca	gtetgtgtaa	tagtagetag	getettagag
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2761	gaagttcaag	gttacaagaa	tgtgagaate	acattigage	atagggaacy	tactgactatt
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3141	gttgaggaag	accaccaayy	agactggctg	gatgatacta	ctgagcaatc	agagattgag
3781	ccagaaccag	aayaayayya	tgaagaacca	gttaatcagt	ttactootta	tttaaaactt
3241	actgacaatg	ttaccattaa	atatattaac	atcottaago	aggcacaaag	tgctaatcct
220I	accountage	Juguatua		5 5 5	55 5	-

			11/90			
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3421	ctcaacaagg	caaccaatgg	tgccatgcaa	aaggagagtg	atgattacat	taagctaaat
3481	ggccctctta	cagtaggagg	gtcttgtttg	ctttctggac	ataatcttgc	taagaagtgt
3541	ctgcatgttg	ttggacctaa	cctaaatgca	ggtgaggaca	tccagcttct	taaggcagca
3601	tatgaaaatt	tcaattcaca	ggacatctta	cttgcaccat	tgttgtcagc	aggcatattt
3661	ggtgctaaac	cacttcagtc	tttacaagtg	tgcgtgcaga	cggttcgtac	acaggtttat
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4621	gtatcatcac	cagatgctgt	tactacatat	aatggatacc	tcacttcgtc	atcaaagaca
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4861	ctaaagagtc	tcttatccct	gcgggaggtt	aagactataa	aagtgttcac	aactgtggac
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5821	accatcaagc	ctgtgtcgta	taaactcgat	ggagttactt	acacagagat	tgaaccaaaa
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10701	tagggggtg	teatecaact	agagatacta	tagatactaa	cctacctctc	cagctaggat
10241	tagagggeeg	tattaactta	gtaggtgtag	cgactggtta	tgttgacact	gaaaataaca
10301	ccccacagg	cacacttaat	gcagecgcac	caccaggtga	ccagtttaaa	catcttatac
10401	gagtaatata	tagageeaac	ccctggaatg	tagtgcgtat	taagatagta	caaatqctca
18421	atastagea	gaaaggettg	tragaragag	tcatattcat	cctttgggcg	catqqctttq
10401	grgatacacc	aataaaatac	tttatcaaga	ttggacctga	aagaacgtgt	tatctatata
10601	agectacace	aacguugtut	tctacttcat	cagatactta	tgcctgctgg	aatcattctg
10601	tagattttaa	ctatototat	aacccattta	tgattgatgt	tcagcagtgg	ggctttacgg
10771	gtaacettca	gagtaaccat	gaccaacatt	gccaggtaca	tggaaatgca	catgtggcta
10721	gtaatcetca	tatcatgact	agatgttag	cagtccatga	gtgctttgtt	aagcgcgttg
10/01	attaatatat	tgaataccct	attataggag	atgaactgag	ggttaattct	gcttgcagaa
10041	accygeeege	cataattata	aagtetgeat	tacttactaa	taagtttcca	gttcttcatg
10061	aagtacaaca	tccaaaggct	atcaagtgtg	tacctcagge	tgaagtagaa	tggaagttct
10001	acattggaaa	accatataat	gacaaagctt	acaaaataga	ggaactcttc	tattcttatg
10001	atagatgetea	coataaatto	actgatgata	tttatttatt	ttggaattgt	aacqttgatc
19001	gttacccacca	caatgcaatt	atatatagat	ttgacacaag	agtcttgtca	aacttgaact
10201	taccage	taataataat	agtttgtatg	tgaataagca	tgcattccac	actccagctt
19201	taccaggeeg	tocatttact	aatttaaagg	aattgccttt	cttttactat	tctgatagtc
10221	. cttataaaag	tcatggcaaa	caagtagtgt	cggatattga	ttatgttcca	ctcaaatctg
10201	ctagggagee	tacacgatgc	aatttaggtg	atactattta	cagacaccat	gcaaatgagt
19301	. ccacgcgcac	cttagataca	tataatatga	tgatttctgc	tggatttagc	ctatggattt
10501	. accgacagta	toatacttat	aacctgtgga	atacatttac	caggttacag	agtttagaaa
10561	atataacaaca	taatattatt	aataaaggag	actttgatgg	acacgccggc	gaagcacctg
10601	tttccatcat	taatgetget	gtttacacaa	aggtagatge	tattgatgtg	gagatetttg
10601	_ ccccaccac	. aacacttcct	gttaatgtto	catttgagct	ttgggctaag	cgtaacatta
107/1	aaaacaayac	agagattaag	ratactcaata	atttagatat	tgatatcgct	gctaatactg
10001	taatctccc	. dydyddiad . ctacaaaaa	gaagccccac	cacatgtate	tacaataggt	gtctgcacaa
10061	taacccyyya taactcacat	taccaadaaa	cctactgaga	atacttatto	ttcacttact	gtcttgtttg
10001	. cyaccyacat Latootagact	. сэвсиидиии	gtagaccttt	ttagaaacgo	ccgtaatggt	gttttaataa
10001	. acygrayago	. agtcaaaggt	ctaacacctt	caaaqqqac	agcacaagct	agcgtcaatg
20041	. cagaaggeee	aattogagaa	tcagtaaaaa	cacaqtttaa	ctactttaag	aaagtagacg
20041	. gagttattat	acagttgcct	gaaacctact	ttactcagac	g cagagactta	gaggatttta
20101	. gcaccacce		. ,		- -	

			agtgagtttg	tagagataga	tatagatasa	ttcatacacc
20161	ageceagace	acaaatggaa	accyaccec	agatagetege	tacggatgaa	agtgatgga
20221	gatataagct	cgagggctat	geettegaae	toggetta	ctggagacccc	tanagnatta
20281	aacttggcgg	tcttcattta	atgatagget	tagecaageg	tteattasts	ccaccaccca
		ttttatccct				
20401	aaacaggttc	atcaaaatgt	grgrgrrcrg	tgattgatet		gactitging
20461	agataataaa	gtcacaagat	ttgtcagtga	tttcaaaagt	ggtcaaggtt	acaattgact
20521	atgctgaaat	ttcattcatg	ctttggtgta	aggatggaca	tgttgaaacc	ttctacccaa
20581	aactacaagc	aagtcaagcg	tggcaaccag	gtgttgcgat	gcctaacttg	tacaagatgc
20641	aaagaatgct	tcttgaaaag	tgtgaccttc	agaattatgg	tgaaaatgct	gttataccaa
20701	aaggaataat	gatgaatgtc	gcaaagtata	ctcaactgtg	tcaatactta	aatacactta
20761	ctttagctgt	accctacaac	atgagagtta	ttcactttgg	tgctggctct	gataaaggag
20821	ttgcaccagg	tacagctgtg	ctcagacaat	ggttgccaac	tggcacacta	cttgtcgatt
20881	cagatcttaa	tgacttcgtc	tccgacgcag	attctacttt	aattggagac	tgtgcaacag
20941	tacatacggc	taataaatgg	gaccttatta	ttagcgatat	gtatgaccct	aggaccaaac
21001	atgtgacaaa	agagaatgac	tctaaagaag	ggtttttcac	ttatctgtgt	ggatttataa
21061	agcaaaaact	agccctgggt	ggttctatag	ctgtaaagat	aacagagcat	tcttggaatg
21121	ctgaccttta	caagcttatg	ggccatttct	catggtggac	agcttttgtt	acaaatgtaa
21181	atgcatcatc	atcggaagca	tttttaattg	gggctaacta	tcttggcaag	ccgaaggaac
21241	aaattgatgg	ctataccatg	catgctaact	acattttctg	gaggaacaca	aatcctatcc
21301	agttgtcttc	ctattcactc	tttgacatga	gcaaatttcc	tcttaaatta	agaggaactg
21361	ctqtaatqtc	tcttaaggag	aatcaaatca	atgatatgat	ttattctctt	ctggaaaaag
21421	gtaggettat	cattagagaa	aacaacagag	ttqtqgtttc	aagtgatatt	cttgttaaca
21481	actaaacgaa	catgtttatt	ttcttattat	ttcttactct	cactagtggt	agtgaccttg
21541	accontacac	cacttttgat	gatgttcaag	ctcctaatta	cactcaacat	acttcatcta
21601	taaaaaaaat	ttactatcct	gatgaaattt	ttagatcaga	cactctttat	ttaactcagg
21661	atttatttct	tccattttat	tctaatqtta	cagggtttca	tactattaat	catacqtttq
21721	gcaaccctgt	catacctttt	aaggatggta	tttattttgc	taccacagag	aaatcaaatq
21721	ttatccataa	ttgggttttt	gattatacca	tgaacaacaa	gtcacagtcg	gtgattatta
21701	ttaacaattc	tactaatgtt	gttatacgag	catgtaactt	tgaattgtgt	gacaaccctt
21011	tetttactat	ttctaaaccc	ataggtacac	agacacatac	tatgatattc	gataatgcat
21001	ttaattggag	tttcgagtac	atatctcatc	ccttttcact	tgatgtttca	gaaaagtcag
21701	ctaattycac	acacttacga	gagttatat	ttaaaaataa	agatgggttt	ctctatgttt
22021	ataagggta	tcaacctata	gagetegege	gtgatctacc	ttctaatttt	aacactttga
22001	acaagggcta	taagttgcct	cttcctatta	acattacaaa	ttttagagcc	attettacag
22141	aacctattt	tgctcaagac	atttgggggg	catcacaaa	acctatttt	attaactatt
22201	cellicace	tacatttatg	attaggggta	atgaaaatgg	tacaatcaca	gatgetate
22261	taaagccaac	tacatttatg	cccaagcacg	acyaaaacyy	tacaaccaca	gacgccgccg
22321	attgttctca	aaatccactt	getgaaetea	ttattagata	agagetet	gagacegaca
22381	aaggaattta	ccagacctct	aattteaggg	Ligitecete	tagtagtage	ttaaattata
22441	ctaatattac	aaacttgtgt	ccttttggag	aggillitaa	tgctactaaa	atactataca
22501	tctatgcatg	ggagagaaaa	addattttta	attgtgttgt	taganatana	ttgaatgatg
22561	actcaacatt	tttttcaacc	tttaagtget	atggegttte	rgccactaag	atangagaaa
22621	tttgcttctc	caatgtctat	gcagattett	ttgtagtcaa	gggagatgat	graayacaaa
22681	tagcgccagg	acaaactggt	gttattgctg	attataatta	taaattgcca	gatgattta
22741	tgggttgtgt	ccttgcttgg	aatactagga	acattgatgc	tacttcaact	ggtaattata
22801	attataaata	taggtatctt	agacatggca	agcttaggcc	ctttgagaga	gacatateta
22861	atgtgccttt	ctcccctgat	ggcaaacctt	gcaccccacc	tgctcttaat	tgttattggc
22921	cattaaatga	ttatggtttt	tacaccacta	ctggcattgg	ctaccaacct	tacagagttg
22981	tagtactttc	ttttgaactt	ttaaatgcac	cggccacggt	ttgtggacca	aaattatcca
23041	ctgaccttat	taagaaccag	tgtgtcaatt	ttaattttaa	tggactcact	ggtactggtg
23101	tgttaactcc	ttcttcaaag	agatttcaac	catttcaaca	atttggccgt	gatgtttctg
23161	atttcactga	ttccgttcga	gatcctaaaa	catctgaaat	attagacatt	tcaccttgct
23221	cttttggggg	tgtaagtgta	attacacctg	gaacaaatgc	ttcatctgaa	gttgctgttc
23281	tatatcaaga	tgttaactgc	actgatgttt	ctacagcaat	tcatgcagat	caactcacac
23341	cagcttggcg	catatattct	actggaaaca	atgtattcca	gactcaagca	ggctgtctta
23401	taggagctga	gcatgtcgac	acttcttatg	agtgcgacat	tcctattgga	gctggcattt
23461	gtgctagtta	ccatacagtt	tctttattac	gtagtactag	ccaaaaatct	attgtggctt

			17/90			
22521	atactatoto	tttaggtgct		ttgcttactc	taataacacc	attqctatac
23521	ctactaactt	ttcaattagc	attactacaq	aagtaatgcc	tgtttctatg	gctaaaacct
23501	ccatagatta	taatatgtac	atctgcggag	attctactga	atgtgctaat	ttgcttctcc
23041	aatatggtag	cttttgcaca	caactaaatc	gtgcactctc	aggtattgct	gctgaacagg
23761	atcocaacac	acgtgaagtg	ttcqctcaag	tcaaacaaat	gtacaaaacc	ccaactttga
23821	aatattttgg	tggttttaat	ttttcacaaa	tattacctga	ccctctaaag	ccaactaaga
23881	ggtctttat	tgaggacttg	ctctttaata	aggtgacact	cgctgatgct	ggcttcatga
23941	agcaatatgg	cgaatgccta	ggtgatatta	atgctagaga	tctcatttgt	gcgcagaagt
24001	tcaatggact	tacagtgttg	ccacctctgc	tcactgatga	tatgattgct	gcctacactg
24061	ctactctaat	tagtggtact	gccactgctg	gatggacatt	tggtgctggc	gctgctcttc
24121	aaataccttt	tgctatgcaa	atggcatata	ggttcaatgg	cattggagtt	acccaaaatg
24181	ttctctatga	qaaccaaaaa	caaatcgcca	accaatttaa	caaggcgatt	agtcaaattc
24241	aagaatcact	tacaacaaca	tcaactgcat	tgggcaagct	gcaagacgtt	gttaaccaga
24301	atgctcaagc	attaaacaca	cttgttaaac	aacttagctc	taattttggt	gcaatttcaa
24361	gtgtgctaaa	tgatatcctt	tcgcgacttg	ataaagtcga	ggcggaggta	caaattgaca
24421	ggttaattac	aggcagactt	caaagccttc	aaacctatgt	aacacaacaa	ctaatcaggg
24481	ctactaaaat	cagggcttct	gctaatcttg	ctgctactaa	aatgtctgag	tgtgttcttg
24541	gacaatcaaa	aagagttgac	ttttgtggaa	agggctacca	ccttatgtcc	ttcccacaag
24601	cageceegea	taatattatc	ttcctacatg	tcacgtatgt	gccatcccag	gagaggaact
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24721	ttgtgtttaa	tggcacttct	tggtttatta	cacagaggaa	CTTCTTTCT	ccacaaataa
24781	ttactacaga	caatacattt	gtctcaggaa	attgtgatgt	cgttattggc	atcattaaca
24841	acacagttta	tgatcctctg	caacctgagc	ttgactcatt	caaagaagag	attaaggatt
24901	actțcaaaaa	tcatacatca	ccagatgttg	atcttggcga	cattleagge	actaacgett
24961	ctgtcgtcaa	cattcaaaaa	gaaattgacc	gcctcaatga	ggccgccaaa	tagacttagt
25021	aatcactcat	tgaccttcaa	gaattgggaa	aatatgagta	catacttaca	atcttacttt
25081	atgtttggct	cggcttcatt	gctggactaa	aggetageta	ctcttataat	tettactaca
25141	gttgcatgac	tagttgttgc	agttgcctca	agggrgcarg	casattacat	tacacataaa
25201	agtttgatga	ggatgactct	gagecagete	tactettees	tcaattacto	cacagccagt
25261	cgaacttatg	gatttgttta	gagacccc	tattcatact	acadcaacda	taccoctaca
25321	aaaaattgac	aatgcttctc	gggtagtat	tagcattaca	tttcttacta	tttttcagag
25381	agcctcactc	cctttcggat ataattgcgc	tcaataaaa	atogcageta	gccctttata	agggcttcca
25441	cgctaccaaa	aatttactgc	tactattat	taccatctat	tcacatcttt	tacttatcac
25501	gttcattige	gaggcgcaat	ttttatacct	ctatgccttg	atatattttc	tacaatqcat
25561	tgcaggtaag	agaattatta	taagatatta	actttattaa	aagtgcaaat	ccaaqaaccc
25621	. caacgcatgt	gatgccaact	actttattta	ctggcacaca	cataactatq	actactgtat
25681	. attacticat	agtgtcacag	atacaattot	cattactaaa	ggtgacggca	tttcaacacc
25/41	. accatataac	gaagactacc	aaattggtgg	ttattctgag	gataggcact	caggtgttaa
25001	. aaaacccaaa	gttgtacatg	gctatttcac	cgaagtttac	taccagettg	agtctacaca
25001	. agaccatgce	gacactggta	ttgaaaatgc	tacattette	atctttaaca	agcttgttaa
25921	agacccacco	aatgtgcaaa	tacacacaat	cgacggctct	tcaggagttg	ctaatccagc
26041	aatggatcca	atttatgatg	agccgacgac	gactactago	gtgcctttgt	aagcacaaga
26101	aagtgagtag	: gaacttatgt	actcattcgt	. ttcggaagaa	acaggtacgt	taatagitaa
26161	tagcgtactt	ctttttcttq	ctttcgtggt	. attcttgcta	ı gtcacactag	ccatccttac
26221	tacacttcaa	ı ttatatacat	actgctgcaa	tattgttaac	: gtgagtttag	taaaaccaac
26281	gatttacato	tactcqcqtq	ttaaaaatct	: gaactcttct	: gaaggagttc	etgatettet
26341	ggtctaaacc	, aactaactat	. tattattatt	. ctgtttggaa	l ctttaacatt	gettateatg
26401	l gcagacaaco	g gtactattac	cqttqaqqaq	, cttaaacaac	: tcctggaaca	atggaaccta
2646	l gtaataggtt	: tcctattcct	aqcctqqatt	: atgttactac	aatttgccta	. ttctaatcyy
26521	l aacaggtttt	totacataat	aaagcttgtt	: ttcctctggc	tcttgtggcc	agtaacactt
2658	l acttatttt	, tacttactat	. tqtctacaga	ı attaattgg <u>g</u>	, tgactggcgg	gattgegatt
2664	l gcaatggctt	gtattqtaqq	r cttgatgtgg	, cttagctact	tegttgette	e etteaggetg
2670	l tttactcata	a cccqctcaat	: qtqqtcattc	: aacccagaaa	a caaacattet	. Leceaacycy
2676	1 cetetecaa	g ggacaattgt	gaccagaccg	g ctcatggaaa	a gtgaacttgt	. carragiger
2682	l gtgatcatto	gtggtcactt	gcgaatggco	ggacactcco	tagggcgctg	tgacattaag

			t-t	+	tttattatta	casattagga
26881	gacctgccaa	aagagatcac	tgtggctaca	ttacgaacge	agagggta	ccatattaga
26941	gegregeage	gtgtaggcac	rgacccaggt	aganagaan	atatteett	actactaca
27001	aactataaat	taaatacaga	ceaegeegge	aycaacyaca	acactgeece	agetattgat
27061	taagtgacaa	cagatgtttc	accitigates	tteeaggit	acaacagcag	taacttcaat
27121	tatcattatg	aggactttca	ggattgctat	reggaatett	taggagettag	atgatgaaga
27181	agtgagacaa	ttatttaagc	ctctaactaa	gaagaactat	toggagetag	atgatgaaga
27241	acctatggag	ttagattatc	cataaaacga	acatgaaaat	tattetette	cegacacega
27301	ttgtatttac	atcttgcgag	ctatatcact	accaggagtg	tgttagaggt	acgaetgtae
27361	tactaaaaga	accttgccca	tcaggaacat	acgagggcaa	ttcaccattt	cacccccccg
27421	ctgacaataa	atttgcacta	acttgcacta	gcacacactt	tgettttget	tgtgetgaeg
27481	gtactcgaca	tacctatcag	ctgcgtgcaa	gatcagtttc	accaaaactt	ttcatcagac
27541	aagaggaggt	tcaacaagag	ctctactcgc	cactttttct	cattgttgct	gctctagtat
27601	ttttaatact	ttgcttcacc	attaagagaa	agacagaatg	aatgagctca	ctttaattga
27661	cttctatttg	tgctttttag	cctttctgct	attccttgtt	ttaataatgc	ttattatatt
27721	ttggttttca	ctcgaaatcc	aggatctaga	agaaccttgt	accaaagtct	aaacgaacat
27781	gaaacttctc	attgttttga	cttgtatttc	tctatgcagt	tgcatatgca	ctgtagtaca
27841	gcgctgtgca	tctaataaac	ctcatgtgct	tgaagatcct	tgtaaggtac	aacactaggg
27901	gtaatactta	tagcactgct	tggctttgtg	ctctaggaaa	ggttttacct	tttcatagat
27961	ggcacactat	ggttcaaaca	tgcacaccta	atgttactat	caactgtcaa	gatccagctg
28021	gtggtgcgct	tatagctagg	tgttggtacc	ttcatgaagg	tcaccaaact	gctgcattta
28081	gagacgtact	tgttgtttta	aataaacgaa	caaattaaaa	tgtctgataa	tggaccccaa
28141	tcaaaccaac	gtagtgcccc	ccgcattaca	tttggtggac	ccacagattc	aactgacaat
28201	aaccagaatg	gaggacgcaa	tggggcaagg	ccaaaacagc	gccgacccca	aggtttaccc
28261	aataatactg	cgtcttggtt	cacagetete	actcagcatg	gcaaggagga	acttagattc
28321	cctcgaggcc	agggcgttcc	aatcaacacc	aatagtggtc	cagatgacca	aattggctac
28381	taccgaagag	ctacccgacg	agttcgtggt	ggtgacggca	aaatgaaaga	gctcagcccc
28441	agatggtact	tctattacct	aggaactggc	ccagaagctt	cacttcccta	cggcgctaac
28501	aaagaaggca	tcgtatgggt	tgcaactgag	ggagccttga	atacacccaa	agaccacatt
28561	ggcacccgca	atcctaataa	caatgctgcc	accgtgctac	aacttcctca	aggaacaaca
28621	ttqccaaaag	gcttctacgc	agagggaagc	agaggcggca	gtcaagcctc	ttctcgctcc
28681	tcatcacgta	gtcgcggtaa	ttcaagaaat	tcaactcctg	gcagcagtag	gggaaattct
28741	cctgctcgaa	tggctagcgg	aggtggtgaa	actgccctcg	cgctattgct	gctagacaga
28801	ttqaaccagc	ttgagagcaa	agtttctggt	aaaggccaac	aacaacaagg	ccaaactgtc
28861	actaagaaat	ctgctgctga	ggcatctaaa	aagcctcgcc	aaaaacgtac	tgccacaaaa
28921	cagtacaacg	tcactcaagc	atttgggaga	cgtggtccag	aacaaaccca	aggaaatttc
28981	ggggaccaag	acctaatcag	acaaggaact	gattacaaac	attggccgca	aattgcacaa
29041	tttgctccaa	gtgcctctgc	attctttgga	atgtcacgca	ttggcatgga	agtcacacct
29101	tcqqqaacat	ggctgactta	tcatggagcc	attaaattgg	atgacaaaga	tccacaattc
29161	aaagacaacg	tcatactgct	gaacaagcac	attgacgcat	acaaaacatt	cccaccaaca
29221	qaqcctaaaa	aggacaaaaa	gaaaaagact	gatgaagctc	agcctttgcc	gcagagacaa
29281	aagaagcagc	ccactgtgac	tcttcttcct	gcggctgaca	tggatgattt	ctccagacaa
29341	cttcaaaatt	ccatgagtgg	agcttctgct	gattcaactc	aggcataaac	actcatgatg
29401	accacacaag	gcagatgggc	tatgtaaacg	ttttcgcaat	tccgtttacg	atacatagtc
29461	tactcttgtg	cagaatgaat	tctcgtaact	aaacagcaca	agtaggttta	gttaacttta
29521	atctcacata	gcaatcttta	atcaatgtgt	aacattaggg	aggacttgaa	agagccacca
29581	cattttcatc	gaggccacgc	ggagtacgat	cgagggtaca	gtgaataatg	ctagggagag
29641	ctgcctatat	ggaagagccc	taatgtgtaa	aattaatttt	agtagtgcta	tccccatgtg
29701	attttaatag	cttcttagga	gaatgacaaa	aaaaaaaaa	aa	
	_					

FIG. 10 Con't

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1 - ATATTAGGTTTTTACCTACCCAGGAAAAGCCAACCACCTCGATCTCTTGTAGATCTGTT - 60
  -ILGFYLPRKSQPTSISCRSV
    Y * V F T Y P G K A N Q P R S L V D L F
     IRFLPTQEKPTNLDLL*ICS
61 - CTCTAAACGAACTTTAAAATCTGTGTAGCTGTCGCTCGGCTGCATGCCTAGTGCACCTAC - 120
  -L * T N F K I C V A V A R L H A * C T Y
    S K R T L K S V * L S L G C M P S A P T
     L N E L * N L C S C R S A A C L V H L R
121 - GCAGTATAAACAATAATAAATTTTACTGTCGTTGACAAGAAACGAGTAACTCGTCCCTCT - 180
   -AV*TIINFTVVDKKRVTRPS
    Q Y K Q * * I L L S L T R N E * L V P L
     SINNNKFYCR*QETSNSSLF
181 - TCTGCAGACTGCTTACGGTTTCGTCCGTGTTGCAGTCGATCATCAGCATACCTAGGTTTC - 240
   -SADCLRFRPCCSRSSAYLGF
    L Q T A Y G F V R V A V D H Q H T * V S
     C R L L T V S S V L Q S I I S I P R F R
241 - GTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTTCTTGGTGTCAACGAGAAAACA - 300
   -VRV*PKGKMESLVLGVNEKT
    S G C D R K V R W R A L F L V S T R K H
     PGVTER*DGEPCSWCQRENT
301 - CACGTCCAACTCAGTTTGCCTGTCCTTCAGGTTAGAGACGTGCTAGTGCGTGGCTTCGGG - 360
   -HVQLSLPVLQVRDVLVRGFG
    TSNSVCLSFRLETC * CVASG
     R P T Q F A C P S G * R R A S A W L R G
361 - GACTCTGTGGAAGAGGCCCTATCGGAGGCACGTGAACACCTCAAAAATGGCACTTGTGGT - 420
   -DSVEEALSEAREHLKNGTCG
    T L W K R P Y R R H V N T S K M A L V V
     L C G R G P I G G T * T P Q K W H L W S
421 - CTAGTAGAGCTGGAAAAAGGCGTACTGCCCCAGCTTGAACAGCCCTATGTGTTCATTAAA - 480
   -LVELEKGVLPQLEQPYVFIK
      * S W K K A Y C P S L N S P M C S L N
    S R A G K R T A P A * T A L·C V H * T
481 - CGTTCTGATGCCTTAAGCACCAATCACGGCCACAAGGTCGTTGAGCTGGTTGCAGAAATG - 540
   -RSDALSTNHGHKVVELVAEM
    V L M P * A P I T A T R S L S W L Q K W
     F * C L K H Q S R P Q G R * A G C R N G
541 - GACGGCATTCAGTACGGTCGTAGCGGTATAACACTGGGAGTACTCGTGCCACATGTGGGC - 600
   -DGIQYGRSGITLGVLVPHVG
    T A F S T V V A V * H W E Y S C H M W A
     R H S V R S * R Y N T G S T R A T C G R
601 - GAAACCCCAATTGCATACCGCAATGTTCTTCTTCGTAAGAACGGTAATAAGGGAGCCGGT - 660
   -ETPIAYRNVLLRKNGNKGAG
   - K P Q L H T A M F F F V R T V I R E P V
     N P N C I P Q C S S S * E R * * G S R W
661 - GGTCATAGCTATGGCATCGATCTAAAGTCTTATGACTTAGGTGACGAGCTTGGCACTGAT - 720
   -G H S Y G I D L K S Y D L G D E L G T D
     \begin{smallmatrix} V & I & A & M & A & S & I & * & S & L & M & T & * & V & T & S & L & A & L & I \\ \end{smallmatrix} 
     S * L W H R S K V L * L R * R A W H * S
721 - CCCATTGAAGATTATGAACAAAACTGGAACACTAAGCATGGCAGTGGTGCACTCCGTGAA - 780
   - PIEDYEQN WNTKHGSGALRE
    P L K I M N K T G T L S M A V V H S V N
     H * R L * T K L E H * A W Q W C T P * T
781 - CTCACTCGTGAGCTCAATGGAGGTGCAGTCACTCGCTATGTCGACAACAATTTCTGTGGC - 840
   -LTRELNGGAVTRYVDNNFCG
   - S L V S S M E V Q S L A M S T T I S V A
     HS*AQWRCSHSLCRQQFLWP
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841 - CCAGATGGGTACCCTCTTGATTGCATCAAAGATTTTCTCGCACGCGCGGGCAAGTCAATG - 900
   - P D G Y P L D C I K D F L A R A G K S M
   - Q M G T L L I A S K I F S H A R A S Q C
    R W V P S * L H Q R F S R T R G Q V N V
901 - TGCACTCTTTCCGAACAACTTGATTACATCGAGTCGAAGAGAGGTGTCTACTGCTGCCGT - 960
   -CTLSEQLDYIESKRGVYCCR
   - A L F P N N L I T S S R R E V S T A A V
    HSFRTT * LHRVEERCLLP *
961 - GACCATGAGCATGAAATTGCCTGGTTCACTGAGCGCTCTGATAAGAGCTACGAGCACCAG - 1020
   -DHEHEIAWFTERSDKSYEHQ
    T M S M K L P G S L S A L I R A T S T R
     P * A * N C L V H * A L * * E L R A P D
1021 - ACACCCTTCGAAATTAAGAGTGCCAAGAAATTTGACACTTTCAAAGGGGAATGCCCAAAG - 1080
   -TPFEIKSAKKFDTFKGECPK
    H P S K L R V P R N L T L S K G N A Q S
     TLRN*ECQEI*HFQRGMPKV
-FVFPLNSKVKVIQPRVEKKK
    L C F L L T Q K S K S F N H V L K R K R
    CVSS*LKSQSHSTTC*KEKD
1141 - ACTGAGGGTTTCATGGGGCGTATACGCTCTGTGTACCCTGTTGCATCTCCACAGGAGTGT - 1200
   -TEGFMGRIRSVYPVASPQEC
   - L R V S W G V Y A L C T L L H L H R S V
    * G F H G A Y T L C V P C C I S T G V *
1201 - AACAATATGCACTTGTCTACCTTGATGAAATGTAATCATTGCGATGAAGTTTCATGGCAG - 1260
   - N N M H L S T L M K C N H C D E V S W Q
   - TICTCLP * * N V I I A M K F H G R
   - QYALVYLDEM*SLR*SFMAD
1261 - ACGTGCGACTTTCTGAAAGCCACTTGTGAACATTGTGGCACTGAAAATTTAGTTATTGAA - 1320
   -TCDFLKATCEHCGTENLVIE
   - RATF * KPLVNIVALKI * LLK
    V R L S E S H L * T L W H * K F S Y * R
1321 - GGACCTACTACATGTGGGTACCTACTACTACTGTGTGAAAATGCCATGTCCTGCC - 1380
   -GPTTCGYLPTNAVVKMPCPA
   - D L L H V G T Y L L M L * * K C H V L P
     T Y Y M W V P T Y * C C S E N A M S C L
1381 - TGTCAAGACCCAGAGATTGGACCTGAGCATAGTGTTGCAGATTATCACAACCACTCAAAC - 1440
   -CODPEIGPEHSVADYHNHSN
    V K T Q R L D L S I V L Q I I T T T Q T
     S R P R D W T * A * C C R L S Q P L K H
1441 - ATTGAAACTCGACTCCGCAAGGGAGGTAGGACTAGATGTTTTGGAGGCTGTGTTTTGCC - 1500
   -IETRLRKGGRTRCFGGCVFA
    L K L D S A R E V G L D V L E A V C L P
     * N S T P Q G R * D * M F W R L C V C L
1501 - TATGTTGGCTGCTATAATAAGCGTGCCTACTGGGTTCCTCGTGCTAGTGCTGATATTGGC - 1560
   - Y V G C Y N K R A Y W V P R A S A D I G
    M L A A I I S V P T G F L V L V L I L A
     C W L L * * A C L L G S S C * C * Y W L
1561 - TCAGGCCATACTGGCATTACTGGTGACAATGTGGAGACCTTGAATGAGGATCTCCTTGAG - 1620
   -SGHTGITGDNVETLNEDLLE
    Q A I L A L L V T M W R P * M R I S L R
     RPYWHYW*QCGDLE*GSP*D
-ILSRERVNINIVGDFHLNEE
   - Y * V V N V L T L T L L A I F I * M K R
     TES*TC*H*HCWRFSFE*RG
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1681 - GTTGCCATCATTTTGGCATCTTTCTCTGCTTCTACAAGTGCCTTTATTGACACTATAAAG - 1740
   -VAIILASFSASTSAFIDTIK
   - L P S F W H L S L L L Q V P L L T L * R
     C H H F G I F L C F Y K C L Y * H Y K E
1741 - AGTCTTGATTACAAGTCTTTCAAAACCATTGTTGAGTCCTGCGGTAACTATAAAGTTACC - 1800
   -SLDYKSFKTIVESCGNYKVT
   - V L I T S L S K P L L S P A V T I K L P
      S * L Q V F Q N H C * V L R * L * S Y Q
1801 - AAGGGAAAGCCCGTAAAAGGTGCTTGGAACATTGGACAACAGAGATCAGTTTTAACACCA - 1860
   - K G K P V K G A W N I G Q Q R S V L T P
    RESP*KVLGTLDNRDQF*HH
      G K A R K R C L E H W T T E I S F N T T
1861 - CTGTGTGGTTTTCCCTCACAGGCTGCTGGTGTTATCAGATCAATTTTTGCGCGCACACTT - 1920
   -LCGFPSQAAGVIRSIFARTL
     C V V F P H R L L V L S D Q F L R A H L
      V W F S L T G C W C Y Q I N F C A H T *
1921 - GATGCAGCAAACCACTCAATTCCTGATTTGCAAAGAGCAGCTGTCACCATACTTGATGGT - 1980
   -DAANHSIPDLQRAAVTILDG
     M Q Q T T Q F L I C K E Q L S P Y L M V
     CSKPLNS*FAKSSCHHT*WY
1981 - ATTTCTGAACAGTCATTACGTCTTGTCGACGCCATGGTTTATACTTCAGACCTGCTCACC - 2040
    -ISEQSLRLVDAMVYTSDLLT
     F L N S H Y V L S T P W F I L Q T C S P
     F * T V I T S C R R H G L Y F R P A H Q
2041 - AACAGTGTCATTATTATGGCATATGTAACTGGTGGTCTTGTACAACAGACTTCTCAGTGG - 2100
   -NSVIIMAYVTGGLVQQTSQW
     T V S L L W H M * L V V L Y N R L L S G
      Q C H Y Y G I C N W W S C T T D F S V V
2101 - TTGTCTAATCTTTTGGGCACTACTGTTGAAAAACTCAGGCCTATCTTTGAATGGATTGAG - 2160
   -LSNLLGTTVEKLRPIFEWIE
     C L I F W A L L L K N S G L S L N G L R
      V * S F G H Y C * K T Q A Y L * M D * G
2161 - GCGAAACTTAGTGCAGGAGTTGAATTTCTCAAGGATGCTTGGGAGATTCTCAAATTTCTC - 2220
    -AKLSAGVEFLKDAWEILKFL
     R N L V Q E L N F S R M L G R F S N F S
      E T * C R S * I S Q G C L G D S Q I S H
2221 - ATTACAGGTGTTTTTGACATCGTCAAGGGTCAAATACAGGTTGCTTCAGATAACATCAAG - 2280
    -ITGVFDIVKGQIQVASDNIK
     L Q V F L T S S R V K Y R L L Q I T S R
      Y R C F * H R Q G S N T G C F R * H Q G
2281 - GATTGTGTAAAATGCTTCATTGATGTTGTTAACAAGGCACTCGAAATGTGCATTGATCAA - 2340
    -DCVKCFIDVVNKALEMCIDQ
     I V * N A S L M L L T R H S K C A L I K
      L C K M L H * C C * Q G T R N V H * S S
2341 - GTCACTATCGCTGGCGCAAAGTTGCGATCACTCAACTTAGGTGAAGTCTTCATCGCTCAA - 2400
    -V T I A G A K L R S L N L G E V F I A Q
     S L S L A Q S C D H S T * V K S S S L K
      HYRWRKVAITQLR*SLHRSK
2401 - AGCAAGGGACTTTACCGTCAGTGTATACGTGGCAAGGAGCAGCTGCAACTACTCATGCCT - 2460
    -SKGLYRQCIRGKEQLQLLMP
     A R D F T V S V Y V A R S S C N Y S C L
      Q G T L P S V Y T W Q G A A A T T H A S
2461 - CTTAAGGCACCAAAAGAAGTAACCTTTCTTGAAGGTGATTCACATGACACAGTACTTACC - 2520
    -L K A P K E V T F L E G D S H D T V L T
     L R H Q K K * P F L K V I H M T Q Y L P
       * G T K R S N L S * R * F T * H S T Y L
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2521 - TCTGAGGAGGTTGTTCTCAAGAACGGTGAACTCGAAGCACTCGAGACGCCCGTTGATAGC - 2580
   -SEEVVLKNGELEALETPVDS
   - L R R L F S R T V N S K H S R P L I A
     * G G C S Q E R * T R S T R D A R * * L
2581 - TTCACAAATGGAGCTATCGTCGGCACACCAGTCTGTGTAAATGGCCTCATGCTCTTAGAG - 2640
   -FTNGAIVGTPVCVNGLMLLE
   - S Q M E L S S A H Q S V * M A S C S * R
      H K W S Y R R H T S L C K W P H A L R D
-I K D K E Q Y C A L S P G L L A T N N V
     L R T K N N T A H C L L V Y W L Q T M S
     * G Q R T I L R I V S W F T G Y K Q C L
2701 - TTTCGCTTAAAAGGGGGTGCACCAATTAAAGGTGTAACCTTTGGAGAAGATACTGTTTGG - 2760
   - F R L K G G A P I K G V T F G E D T V W
     FA * KG V H Q L K V * P L E K I L F G
     S L K R G C T N * R C N L W R R Y C L G
2761 - GAAGTTCAAGGTTACAAGAATGTGAGAATCACATTTGAGCTTGATGAACGTGTTGACAAA - 2820
   -EVQGYKNVRITFELDERVDK
     K F K V T R M * E S H L S L M N V L T K
      S S R L Q E C E N H I * A * * T C * Q S
2821 - GTGCTTAATGAAAAGTGCTCTGTCTACACTGTTGAATCCGGTACCGAAGTTACTGAGTTT - 2880
   -VLNEKCSVYTVESGTEVTEF
     C L M K S A L S T L L N P V P K L L S L
   - A * * K V L C L H C * I R Y R S Y * V C
2881 - GCATGTGTTGTAGCAGAGGCTGTTGTGAAGACTTTACAACCAGTTTCTGATCTCCTTACC - 2940
   - A C V V A E A V V K T L Q P V S D L L T
   - H V L * Q R L L * R L Y N Q F L I S L P
   - MCCSRGCCEDFTTSF * SPYQ
2941 - AACATGGGTATTGATCTTGATGAGTGGAGTGTAGCTACATTCTACTTATTTGATGATGCT - 3000
   -NMGIDLDEWSVATFYLFDDA
      \begin{smallmatrix} T & W & V & L & I & L & M & S & G & V & * & L & H & S & T & Y & L & M & M & L \\ \end{smallmatrix} 
   - HGY*S**VECSYILLI**CW
3001 - GGTGAAGAAACTTTTCATCACGTATGTATTGTTCCTTTTACCCTCCAGATGAGGAAGAA - 3060
   -GEENFSSRMYCSFYPPDEEE
     V K K T F H H V C I V P F T L Q M R K K
      * R K L F I T Y V L F L L P S R * G R R
3061 - GAGGACGATGCAGAGTGTGAGGAAGAAGAAATTGATGAAACCTGTGAACATGAGTACGGT - 3120
   -EDDAECEEEIDETCEHEYG
   - R T M Q S V R K K L M K P V N M S T V
     GRCRV*GRRN**NL*T*VRY
3121 - ACAGAGGATGATTATCAAGGTCTCCCTCTGGAATTTGGTGCCTCAGCTGAAACAGTTCGA - 3180
   -TEDDYQGLPLEFGASAETVR
      \begin{smallmatrix} Q & R & M & I & I & K & V & S & L & W & N & L & V & P & Q & L & K & Q & F & E \\ \end{smallmatrix} 
      RG * L S R S P S G I W C L S * N S S S
3181 - GTTGAGGAAGAAGAAGAGAGACTGGCTGGATGATACTACTGAGCAATCAGAGATTGAG - 3240
   -VEEEEEDWLDDTTEQSEIE
    LRKKKRKTGWMILLSNQRLS
      * G R R G R L A G * Y Y * A I R D * A
3241 - CCAGAACCAGAACCTACACCTGAAGAACCAGTTAATCAGTTTACTGGTTATTTAAAACTT - 3300
   -PEPEPTPEEPVNQFTGYLKL
     Q N Q N L H L K N Q L I S L L V I * N L
      RTRTYT*RTS*SVYWLFKTY
3301 - ACTGACAATGTTGCCATTAAATGTGTTGACATCGTTAAGGAGGCACAAAGTGCTAATCCT - 3360
   -TDNVAIKCVDIVKEAQSANP
   - L T M L P L N V L T S L R R H K V L I L
      * Q C C H * M C * H R * G G T K C * S Y
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3361 - ATGGTGATTGTAAATGCTGCTAACATACACCTGAAACATGGTGGTGGTGTAGCAGGTGCA - 3420
   - M V I V N A A N I H L K H G G G V A G A
   - W * L * M L L T Y T * N M V V V * Q V H
      G D C K C C * H T P E T W W W C S R C T
3421 - CTCAACAAGGCAACCAATGGTGCCATGCAAAAGGAGAGTGATGATTACATTAAGCTAAAT - 3480
   -LNKATNGAMQKESDDYIKLN
   - S T R Q P M V P C K R R V M I T L S * M
      Q Q G N Q W C H A K G E * * L H * A K W
3481 - GGCCCTCTTACAGTAGGAGGGTCTTGTTTGCTTTCTGGACATAATCTTGCTAAGAAGTGT - 3540
   -GPLTVGGSCLLSGHNLAKKC
   - A L L Q * E G L V C F L D I I L L R S V
     PSYSRRVLFAFWT*SC*EVS
3541 - CTGCATGTTGTTGGACCTAAACCTAAATGCAGGTGAGGACATCCAGCTTCTTAAGGCAGCA - 3600
   - L H V V G P N L N A G E D I Q L L K A A
     C M L L D L T * M Q V R T S S F L R Q H
     ACCWT*PKCR*GHPAS*GSI
3601 - TATGAAAATTTCAATTCACAGGACATCTTACTTGCACCATTGTTGTCAGCAGGCATATTT - 3660
   -YENFNSQDILLAPLLSAGIF
     M K I S I H R T S Y L H H C C Q Q A Y L
     * K F Q F T G H L T C T I V V S R H I W
3661 - GGTGCTAAACCACTTCAGTCTTTACAAGTGTGCGTGCAGACGGTTCGTACACAGGTTTAT - 3720
   -GAKPLQSLQVCVQTVRTQVY
     V L N H F S L Y K C A C R R F V H R F I
      C * T T S V F T S V R A D G S Y T G L Y
3721 - ATTGCAGTCAATGACAAAGCTCTTTATGAGCAGGTTGTCATGGATTATCTTGATAACCTG - 3780
   -IAVNDKALYEQVVMDYLDNL
     LQSMTKLFMSRLSWIILIT*
      CSQ*QSSL*AGCHGLS**PE
3781 - AAGCCTAGAGTGGAAGCACCTAAACAAGAGGGGCCACCAAACACAGAAGATTCCAAAACT - 3840
   - K P R V E A P K Q E E P P N T E D S K T
   - S L E W K H L N K R S H Q T Q K I P K L
   - A * S G S T * T R G A T K H R R F Q N *
3841 - GAGGAGAAATCTGTCGTACAGAAGCCTGTCGATGTGAAGCCAAAAATTAAGGCCTGCATT - 3900
    -EEKSVVQKPVDVKPKIKACI
   - R R N L S Y R S L S M * S Q K L R P A L
   - GEICRTEACRCEAKN * GLH *
3901 - GATGAGGTTACCACAACACTGGAAGAAACTAAGTTTCTTACCAATAAGTTACTCTTGTTT - 3960
    -DEVTTLEETKFLTNKLLLF
   - M R L P Q H W K K L S F L P I S Y S C L
    - * G Y H N T G R N * V S Y Q * V T L V C
3961 - GCTGATATCAATGGTAAGCTTTACCATGATTCTCAGAACATGCTTAGAGGTGAAGATATG - 4020
   - A D I N G K L Y H D S Q N M L R G E D M
- L I S M V S F T M I L R T C L E V K I C
     * Y Q W * A L P * F S E H A * R * R Y V
4021 - TCTTTCCTTGAGAAGGATGCACCTTACATGGTAGGTGATGTTATCACTAGTGGTGATATC - 4080
    -SFLEKDAPYMVGDVITSGDI
    - L S L R R M H L T W * V M L S L V V I S
      FP*EGCTLHGR*CYH*W*YH
4081 - ACTTGTGTTGTAATACCCTCCAAAAAGGCTGGTGGCACTACTGAGATGCTCTCAAGAGCT - 4140
    -TCVVIPSKKAGGTTEMLSRA
    L V L * Y P P K R L V A L L R C S Q E L
     L C C N T L Q K G W W H Y * D A L K S F
4141 - TTGAAGAAAGTGCCAGTTGATGAGTATATAACCACGTACCCTGGACAAGGATGTGCTGGT - 4200
    - L K K V P V D E Y I T T Y P G Q G C A G
     * R K C Q L M S I * P R T L D K D V L V
     E E S A S * * V Y N H V P W T R M C W L
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4201 - TATACACTTGAGGAAGCTAAGACTGCTCTTAAGAAATGCAAATCTGCATTTTATGTACTA - 4260
   - Y T L E E A K T A L K K C K S A F Y V L
   - I H L R K L R L L L R N A N L H F M Y Y
     Y T * G S * D C S * E M Q I C I L C T T
4261 - CCTTCAGAAGCACCTAATGCTAAGGAAGAGATTCTAGGAACTGTATCCTGGAATTTGAGA - 4320
   - P S E A P N A K E E I L G T V S W N L R
   - L Q K H L M L R K R F * E L Y P G I * E
      FRST * C * G R D S R N C I L E F E R
4321 - GAAATGCTTGCTCATGCTGAAGAGACAAGAAAATTAATGCCTATATGCATGGATGTTAGA - 4380
   -E M L A H A E E T R K L M P I C M D V R
    KCLLMLKRQEN*CLYAWMLE
     NACSC*RDKKINAYMHGC*S
4381 - GCCATAATGGCAACCATCCAACGTAAGTATAAAGGAATTAAAATTCAAGAGGGCATCGTT - 4440
   - A I M A T I Q R K Y K G I K I Q E G I V
     P * W Q P S N V S I K E L K F K R A S L
      HNGNHPT * V * RN * NS RGHR *
4441 - GACTATGGTGTCCGATTCTTCTTTTATACTAGTAAAGAGCCTGTAGCTTCTATTATTACG - 4500
   -DYGVRFFFYTSKEPVASIIT
     T M V S D S S F I L V K S L * L L L R
     L W C P I L L Y * * R A C S F Y Y Y E
4501 - AAGCTGAACTCTCTAAATGAGCCGCTTGTCACAATGCCAATTGGTTATGTGACACATGGT - 4560
   -KLNSLNEPLVTMPIGYVTHG
     S * T L * M S R L S Q C Q L V M * H M V
     A E L S K * A A C H N A N W L C D T W F
4561 - TTTAATCTTGAAGAGGCTGCGCGCTGTATGCGTTCTCTTAAAGCTCCTGCCGTAGTGTCA - 4620
   - F N L E E A A R C M R S L K A P A V V S
     LILKRLRAVCVLLKLLP*CQ
     * S * R G C A L Y A F S * S S C R S V S
4621 - GTATCATCACCAGATGCTGTTACTACATATAATGGATACCTCACTTCGTCATCAAAGACA - 4680
   -V S S P D A V T T Y N G Y L T S S S K T
     Y H H Q M L L L H I M D T S L R H Q R H
      I I T R C C Y Y I * W I P H F V I K D I
-SEEHFVETVSLAGSYRDWSY
   - L R S T L * K Q F L W L A L T E I G P I
   - * G A L C R N S F F G W L L Q R L V L F
4741 - TCAGGACAGCGTACAGAGTTAGGTGTTGAATTTCTTAAGCGTGGTGACAAAATTGTGTAC - 4800
   -SGQRTELGVEFLKRGDKIVY
     Q D S V Q S * V L N F L S V V T K L C T
      RTAYRVRC*IS*AW*QNCVP
4801 - CACACTCTGGAGAGCCCCGTCGAGTTTCATCTTGACGGTGAGGTTCTTTCACTTGACAAA - 4860
    -HTLESPVEFHLDGEVLSLDK
     T L W R A P S S F I L T V R F F H L T N
      H S G E P R R V S S * R * G S F T * Q T
4861 - CTAAAGAGTCTCTTATCCCTGCGGGAGGTTAAGACTATAAAAGTGTTCACAACTGTGGAC - 4920
    -LKSLLSLREVKTIKVFTTVD
      * R V S Y P C G R L R L * K C S Q L W T
      KESLIPAGG*DYKSVHNCGQ
4921 - AACACTAATCTCCACACACAGCTTGTGGATATGTCTATGACATATGGACAGCAGTTTGGT - 4980
    -NTNLHTQLVDMSMTYGQQFG
     TLISTHSLWICL*HMDSSLV
      H * S P H T A C G Y V Y D I W T A V W S
4981 - CCAACATACTTGGATGGTGCTGATGTTACAAAAATTAAACCTCATGTAAATCATGAGGGT - 5040
    - P T Y L D G A D V T K I K P H V N H E G
     Q H T W M V L M L Q K L N L M * I M R V
      NILGWC * CYKN * TSCKS * G *
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5041 - AAGACTTTCTTTGTACTACCTAGTGATGACACACTACGTAGTGAAGCTTTCGAGTACTAC - 5100
   -KTFFVLPSDDTLRSEAFEYY
   - R L S L Y Y L V M T H Y V V K L S S T T
    D F L C T T * * * H T T * * S F R V L P
5101 - CATACTCTTGATGAGAGTTTTCTTGGTAGGTACATGTCTGCTTTAAACCACACAAAGAAA - 5160
   -HTLDESFLGRYMSALNHTKK
    ILLMRVFLVGTCLL*TTQRN
     YS**EFSW*VHVCFKPHKEM
5161 - TGGAAATTTCCTCAAGTTGGTGGTTTAACTTCAATTAAATGGGCTGATAACAATTGTTAT - 5220
   -W K F P Q V G G L T S I K W A D N N C Y
   - G N F L K L V V * L Q L N G L I T I V I
     EISSSWWFNFN*MG**QLLF
5221 - TTGTCTAGTGTTTTATTAGCACTTCAACAGCTTGAAGTCAAATTCAATGCACCAGCACTT - 5280
   -LSSVLLALQQLEVKFNAPAL
    C L V F Y * H F N S L K S N S M H Q H F
     V * C F I S T S T A * S Q I Q C T S T S
5281 - CAAGAGGCTTATTATAGAGCCCGTGCTGGTGATGCTGCTAACTTTTGTGCACTCATACTC - 5340
   -QEAYYRARAGDAANFCALIL
     K R L I I E P V L V M L L T F V H S Y S
    RGLL*SPCW*CC*LLCTHTR
5341 - GCTTACAGTAATAAAACTGTTGGCGAGCTTGGTGATGTCAGAGAAACTATGACCCATCTT - 5400
   -AYSNKTVGELGDVRETMTHL
    L T V I K L L A S L V M S E K L * P I F
     L Q * * N C W R A W * C Q R N Y D P S S
5401 - CTACAGCATGCTAATTTGGAATCTGCAAAGCGAGTTCTTAATGTGGTGTGTAAACATTGT - 5460
   -LQHANLESAKRVLNVVCKHC
     Y S M L I W N L Q S E F L M W C V N I V
     TAC*FGICKASS*CGV*TLW
5461 - GGTCAGAAAACTACTACCTTAACGGGTGTAGAAGCTGTGATGTATATGGGTACTCTATCT - 5520
   -GQKTTTLTGVEAVMYMGTLS
     V R K L L P * R V * K L * C I W V L Y L
     S E N Y Y L N G C R S C D V Y G Y S I L
- Y D N L K T G V S I P C V C G R D A T Q
   - MIILRQVFPFHVCVVMLHN
   - * * S * D R C F H S M C V W S * C Y T I
5581 - TATCTAGTACAACAAGAGTCTTCTTTTGTTATGATGTCTGCACCACCTGCTGAGTATAAA - 5640
   - Y L V Q Q E S S F V M M S A P P A E Y K
    I * Y N K S L L L * C L H H L L S I N
     SSTTRVFFCYDVCTTC*V*I
5641 - TTACAGCAAGGTACATTCTTATGTGCGAATGAGTACACTGGTAACTATCAGTGTGGTCAT - 5700
   -LQQGTFLCANEYTGNYQCGH
     Y S K V H S Y V R M S T L V T I S V V I
      TARYILMCE * V H W * L S V W S L
5701 - TACACTCATATAACTGCTAAGGAGACCCTCTATCGTATTGACGGAGCTCACCTTACAAAG - 5760
   - Y T H I T A K E T L Y R I D G A H L T K
     T L I * L L R R P S I V L T E L T L Q R
     H S Y N C * G D P L S Y * R S S P Y K D
5761 - ATGTCAGAGTACAAAGGACCAGTGACTGATGTTTTCTACAAGGAAACATCTTACACTACA - 5820
   - M S E Y K G P V T D V F Y K E T S Y T T
     C Q S T K D Q * L M F S T R K H L T L Q
      V R V Q R T S D * C F L Q G N I L H Y N
-TIKPVSYKLDGVTYTEIEPK
     PSSLCRINSMELLTQRLNQN
      HQACVV*TRWSYLHRD*TKI
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5881 - TTGGATGGGTATTATAAAAAGGATAATGCTTACTATACAGAGCAGCCTATAGACCTTGTA - 5940
   -LDGYYKKDNAYYTEQPIDLV
   - W M G I I K R I M L T I Q S S L * T L Y
     G W V L * K G * C L L Y R A A Y R P C T
5941 - CCAACTCAACCATTACCAAATGCGAGTTTTGATAATTTCAAACTCACATGTTCTAACACA - 6000
   -PTQPLPNASFDNFKLTCSNT
    Q L N H Y Q M R V L I I S N S H V L T Q
    NSTITKCEF**FQTHMF*HK
6001 - AAATTTGCTGATGATTTAAATCAAATGACAGGCTTCACAAAGCCAGCTTCACGAGAGCTA - 6060
   -KFADDLNQMTGFTKPASREL
    N L L M I * I K * Q A S Q S Q L H E S Y
      I C * * F K S N D R L H K A S F T R A I
6061 - TCTGTCACATTCTTCCCAGACTTGAATGGCGATGTAGTGGCTATTGACTATAGACACTAT - 6120
   -SVTFFPDLNGDVVAIDYRHY
    LSHSSQT * MAM * WLLTIDTI
     CHILPRLEWRCSGY*L*TLF
6121 - TCAGCGAGTTTCAAGAAAGGTGCTAAATTACTGCATAAGCCAATTGTTTGGCACATTAAC - 6180
   -SASFKKGAKLLHKPIVWHIN
     Q R V S R K V L N Y C I S Q L F G T L T
      SEFQERC*ITA*ANCLAH*P
6181 - CAGGCTACAACCAAGACAACGTTCAAACCAAACACTTGGTGTTTACGTTGTCTTTGGAGT - 6240
   -QATTKTFKPNTWCLRCLWS
     R L Q P R Q R S N Q T L G V Y V V F G V
      G Y N Q D N V Q T K H L V F T L S L E Y
6241 - ACAAAGCCAGTAGATACTTCAAATTCATTTGAAGTTCTGGCAGTAGAAGACACACAAGGA - 6300
   -TKPVDTSNSFEVLAVEDTQG
     Q S Q * I L Q I H L K F W Q * K T H K E
      KASRYFKFI*SSGSRRHTRN
6301 - ATGGACAATCTTGCTTGTGAAAGTCAACAACCCACCTCTGAAGAAGTAGTGGAAAAATCCT - 6360
   - M D N L A C E S Q Q P T S E E V V E N P
     W T I L L V K V N N P P L K K * W K I L
      G Q S C L * K S T T H L * R S S G K S Y
6361 - ACCATACAGAAGGAAGTCATAGAGTGTGACGTGAAAACTACCGAAGTTGTAGGCAATGTC - 6420
   -TIQKEVIECDVKTTEVVGNV
   - PYRRKS * SVT * KLPKL * AMS
      H T E G S H R V * R E N Y R S C R Q C H
6421 - ATACTTAAACCATCAGATGAAGGTGTTAAAGTAACACAAGAGTTAGGTCATGAGGATCTT - 6480
   -ILKPSDEGVKVTQELGHEDL
     Y L N H Q M K V L K * H K S * V M R I L
      T * T I R * R C * S N T R V R S * G S Y
6481 - ATGGCTGCTTATGTGGAAAACACAAGCATTACCATTAAGAAACCTAATGAGCTTTCACTA - 6540
   - M A A Y V E N T S I T I K K P N E L S L
     G C L C G K H K H Y H * E T * * A F T S
6541 - GCCTTAGGTTTAAAAACAATTGCCACTCATGGTATTGCTGCAATTAATAGTGTTCCTTGG - 6600
   -ALGLKTIATHGIAAINSVPW
     P * V * K Q L P L M V L L Q L I V F L G
      L R F K N N C H S W Y C C N * * C S L E
6601 - AGTAAAATTTTGGCTTATGTCAAACCATTCTTAGGACAAGCAGCAATTACAACATCAAAT - 6660
   -SKILAYVKPFLGQAAITTSN
     V K F W L M S N H S * D K Q Q L Q H Q I
      * N F G L C Q T I L R T S S N Y N I K L
6661 - TGCGCTAAGAGATTAGCACAACGTGTGTTTAACAATTATATGCCTTATGTGTTTACATTA - 6720
   -CAKRLAQRVFNNYMPYVFTL
   - A L R D * H N V C L T I I C L M C L H Y
      R * E I S T T C V * Q L Y A L C V Y I I
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6721 - TTGTTCCAATTGTGTACTTTTACTAAAAGTACCAATTCTAGAATTAGAGCTTCACTACCT - 6780
   -LFQLCTFTKSTNSRIRASLP
   - C S N C V L L K V P I L E L H Y L
     V P I V Y F Y * K Y Q F * N * S F T T Y
6781 - ACAACTATTGCTAAAAATAGTGTTAAGAGTGTTGCTAAATTATGTTTGGATGCCGGCATT - 6840
   -TTIAKNSVKSVAKLCLDAGI
   - Q L L K I V L R V L L N Y V W M P A L
     NYC * K * C * E C C * I M F G C R H *
6841 - AATTATGTGAAGTCACCCAAATTTTCTAAATTGTTCACAATCGCTATGTGGCTATTGTTG - 6900
   -NYVKSPKFSKLFTIAMWLLL
     I M * S H P N F L N C S Q S L C G Y C C
      L C E V T Q I F * I V H N R Y V A I V V
6901 - TTAAGTATTTGCTTAGGTTCTCTAATCTGTGTAACTGCTGCTTTTTGGTGTACTCTTATCT - 6960
   -LSICLGSLICVTAAFGVLLS
      V F A * V L * S V * L L L V Y S Y L
      KYLLRFSNLCNCCFWCTLI*
6961 - AATTTTGGTGCTCCTTCTTATTGTAATGGCGTTAGAGAATTGTATCTTAATTCGTCTAAC - 7020
   -N F G A P S Y C N G V R E L Y L N S S N
     I L V L L I V M A L E N C I L I R L T
      FWCSFLL*WR*RIVS*FV*R
7021 - GTTACTACTATGGATTTCTGTGAAGGTTCTTTTCCTTGCAGCATTTGTTTAAGTGGATTA - 7080
   -V T T M D F C E G S F P C S I C L S G L
     L L L W I S V K V L F L A A F V * V D *
     YYYGFL*RFFSLQHLFKWIR
7081 - GACTCCCTTGATTCTTATCCAGCTCTTGAAACCATTCAGGTGACGATTTCATCGTACAAG - 7140
   -DSLDSYPALETIQVTISSYK
-TPLILIQLLKPFR*RFHRTS
     LP*FLSSS*NHSGDDFIVQA
7141 - CTAGACTTGACAATTTTAGGTCTGGCCGCTGAGTGGGTTTTGGCATATATGTTGTTCACA - 7200
   - L D L T I L G L A A E W V L A Y M L F T
- * T * Q F * V W P L S G F W H I C C S Q
- R L D N F R S G R * V G F G I Y V V H K
7201 - AAATTCTTTTATTTATTAGGTCTTTCAGCTATAATGCAGGTGTTCTTTGGCTATTTTGCT - 7260
   -K F F Y L L G L S A I M Q V F F G Y F A
   - N S F I Y * V F Q L * C R C S L A I L L
      ILLFIRSFSYNAGVLWLFC*
7261 - AGTCATTTCATCAGCAATTCTTGGCTCATGTGGTTTATCATTAGTATTGTACAAATGGCA - 7320
   -SHFISNSWLMWFIISIVQMA
     S F H Q Q F L A H V V Y H * Y C T N G T
-PVSAMVRMYIFFASFYYIWK
     PFLQWLGCTSSLLLSTTYGR
      R F C N G * D V H L L C F F L L H M E E
7381 - AGCTATGTTCATATCATGGATGGTTGCACCTCTTCGACTTGCATGATGTGCTATAAGCGC - 7440
   - S Y V H I M D G C T S S T C M M C Y K R
     A M F I S W M V A P L R L A * C A I S A
      LCSYHGWLHLFDLHDVL*AQ
7441 - AATCGTGCCACACGCGTTGAGTGTACAACTATTGTTAATGGCATGAAGAGATCTTTCTAT - 7500
    -NRATRVECTTIVNGMKRSFY
     I V P H A L S V Q L L L M A * R D L S M
      S C H T R * V Y N Y C * W H E E I F L C
7501 - GTCTATGCAAATGGAGGCCGTGGCTTCTGCAAGACTCACAATTGGAATTGTCTCAATTGT - 7560
    - V Y A N G G R G F C K T H N W N C L N C
     S M Q M E A V A S A R L T I G I V S I V
      LCKWRPWLLQDSQLELSQL*
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7561 - GACACATTTTGCACTGGTAGTACATTCATTAGTGATGAAGTTGCTCGTGATTTGTCACTC - 7620
   -DTFCTGSTFISDEVARDLSL
   - T H F A L V V H S L V M K L L V I C H S
     H I L H W * Y I H * * * S C S * F V T P
7621 - CAGTTTAAAAGACCAATCAACCCTACTGACCAGTCATCGTATATTGTTGATAGTGTTGCT - 7680
   -QFKRPINPTDQSSYIVDSVA
   - S L K D Q S T L L T S H R I L L I V L L
     V * K T N Q P Y * P V I V Y C * * C C C
7681 - GTGAAAAATGGCGCGCTTCACCTCTACTTTGACAAGGCTGGTCAAAAGACCTATGAGAGA - 7740
   - V K N G A L H L Y F D K A G Q K T Y E R
      K M A R F T S T L T R L V K R P M R D
      EKWRASPLL * QGWSKDL * ET
7741 - CATCCGCTCTCCCATTTTGTCAATTTAGACAATTTGAGAGCTAACACACTAAAGGTTCA - 7800
   - H P L S H F V N L D N L R A N N T K G S
     IRSPILSI*TI*ELTTLKVH
      SALPFCQFRQFES*QH*RFT
7801 - CTGCCTATTAATGTCATAGTTTTTGATGGCAAGTCCAAATGCGACGAGTCTGCTTCTAAG - 7860
   -LPINVIVFDGKSKCDESASK
     C L L M S * F L M A S P N A T S L L L S
      A Y * C H S F * W Q V Q M R R V C F * V
7861 - TCTGCTTCTGTGTACTACAGTCAGCTGATGTGCCAACCTATTCTGTTGCTTGACCAAGCT - 7920
   -SASVYYSQLMCQPILLLDQA
   - L L C T T V S * C A N L F C C L T K L
      C F C V L Q S A D V P T Y S V A * P S S
7921 - CTTGTATCAAACGTTGGAGATAGTACTGAAGTTTCCGTTAAGATGTTTGATGCTTATGTC - 7980
   -L V S N V G D S T E V S V K M F D A Y V
   -.LYQTLEIVLKFPLRCLMLMS
   - CIKRWR*Y*SFR*DV*CLCR
7981 - GACACCTTTTCAGCAACTTTTAGTGTTCCTATGGAAAAACTTAAGGCACTTGTTGCTACA - 8040
   -D T F S A T F S V P M E K L K A L V A T
     T P F Q Q L L V F L W K N L R H L L L Q
      H L F S N F * C S Y G K T * G T C C Y S
8041 - GCTCACAGCGAGTTAGCAAAGGGTGTAGCTTTAGATGGTGTCCTTTCTACATTCGTGTCA - 8100
   -AHSELAKGVALDGVLSTFVS
   - L T A S * Q R V * L * M V S F L H S C Q
- S Q R V S K G C S F R W C P F Y I R V S
8101 - GCTGCCCGACAAGGTGTTGTTGATACCGATGTTGACACAAAGGATGTTATTGAATGTCTC - 8160
   - A A R Q G V V D T D V D T K D V I E C L
     C P T R C C * Y R C * H K G C Y * M S Q
8161 - AAACTTTCACATCACTCTGACTTAGAAGTGACAGGTGACAGTTGTAACAATTTCATGCTC - 8220
   -KLSHHSDLEVTGDSCNNFML
     N F H I T L T * K * Q V T V V T I S C S
      TFTSL*LRSDR*QL*QFHAH
8221 - ACCTATAATAAGGTTGAAAACATGACGCCCAGAGATCTTGGCGCATGTATTGACTGTAAT - 8280
   -TYNKVENMTPRDLGACIDCN
     PIIRLKT * RPEILAHVLTVM
      L * * G * K H D A Q R S W R M Y * L * C
8281 - GCAAGGCATATCAATGCCCAAGTAGCAAAAAGTCACAATGTTTCACTCATCTGGAATGTA - 8340
   -ARHINAQVAKSHNVSLIWNV
     Q G I S M P K * Q K V T M F H S S G M *
      KAYQCPSSKKSQCFTHLECK
8341 - AAAGACTACATGTCTTTATCTGAACAGCTGCGTAAACAAATTCGTACTGCTGCCAAGAAG - 8400
   - K D Y M S L S E Q L R K Q I R T A A K K
    KTTCLYLNSCVNKFVLLPR
      R L H V F I * T A A * T N S Y C C Q E E
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8401 - AACAACATACCTTTTACACTAACTTGTGCTACAACTAGACAGGTTGTCAATGTCATAACT - 8460
   -NNIPFTLTCATTRQVVNVIT
   - T T Y L L H * L V L Q L D R L S M S * L
      Q H T F Y T N L C Y N * T G C Q C H N Y
8461 - ACTAAAATCTCACTCAAGGGTGGTAAGATTGTTAGTACTTGTTTTAAACTTATGCTTAAG - 8520
   -T K I S L K G G K I V S T C F K L M L K
   - L K S H S R V V R L L V L V L N L C L R
      * N L T Q G W * D C * Y L F * T Y A * G
-ATLLCVLAALVCYIVMPVHT
     PHYCAFLLHWFVISLCQYIH
      H I I V R S C C I G L L Y R Y A S T Y I
8581 - TTGTCAATCCATGATGGTTACACAAATGAAATCATTGGTTACAAAGCCATTCAGGATGGT - 8640
    -LSIHDGYTNEIIGYKAIQDG
       Q S M M V T Q M K S L V T K P F R M V
      V N P * W L H K * N H W L Q S H S G W C
8641 - GTCACTCGTGACATCATTTCTACTGATGATTGTTTTGCAAATAAACATGCTGGTTTTGAC - 8700
    -V T R D I I S T D D C F A N K H A G F D
     S L V T S F L L M I V L Q I N M L V L T
     H S * H H F Y * * L F C K * T C W F * R
8701 - GCATGGTTTAGCCAGCGTGGTGGTTCATACAAAATGACAAAAGCTGCCCTGTAGTAGCT - 8760
    - A W F S Q R G G S Y K N D K S C P V V A
    - H G L A S V V V H T K M T K A A L * * L
    - MV * PAWWFIQK * QKLPCSSC
8761 - GCTATCATTACAAGAGAGTTGGTTTCATAGTGCCTGGCTTACCGGGTACTGTGCTGAGA - 8820
    -AIITREIGFIVPGLPGTVLR
    - L S L Q E R L V S * C L A Y R V L C * E
      Y H Y K R D W F H S A W L T G Y C A E S
8821 - GCAATCAATGGTGACTTCTTGCATTTTCTACCTCGTGTTTTTAGTGCTGTTTGGCAACATT - 8880
    -AING D F L H F L P R V F S A V G N I
       \begin{smallmatrix} \mathsf{Q} \end{smallmatrix} \ \mathsf{S} \ \mathsf{M} \ \mathsf{V} \ \mathsf{T} \ \mathsf{S} \ \mathsf{C} \ \mathsf{I} \ \mathsf{F} \ \mathsf{Y} \ \mathsf{L} \ \mathsf{V} \ \mathsf{F} \ \mathsf{L} \ \mathsf{V} \ \mathsf{L} \ \mathsf{L} \ \mathsf{A} \ \mathsf{T} \ \mathsf{F} 
      N Q W * L L A F S T S C F * C C W Q H L
8881 - TGCTACACACCTTCCAAACTCATTGAGTATAGTGATTTTGCTACCTCTGCTTGCGTTCTT - 8940
    -CYTPSKLIEYSDFATSACVL
    - A T H L P N S L S I V I L L P L L A F L
      L H T F Q T H * V * * F C Y L C L R S C
8941 - GCTGCTGAGTGTACAATTTTTAAGGATGCTATGGGCAAACCTGTGCCATATTGTTATGAC - 9000
    - A A E C T I F K D A M G K P V P Y C Y D
     LLSVQFLRMLWANLCHIVMT
       C * V Y N F * G C Y G Q T C A I L L * H
9001 - ACTAATTTGCTAGAGGGTTCTATTTCTTATAGTGAGCTTCGTCCAGACACTCGTTATGTG - 9060
    -TNLLEGSISYSELRPDTRYV
     9061 - CTTATGGATGGTTCCATCATACAGTTTCCTAACACTTACCTGGAGGGTTCTGTTAGAGTA - 9120
    -L M D G S I I Q F P N T Y L E G S V R V
      L W M V P S Y S F L T L T W R V L L E *
       Y G W F H H T V S * H L P G G F C * S S
9121 - GTAACAACTTTTGATGCTGAGTACTGTAGACATGGTACATGCGAAAGGTCAGAAGTAGGT - 9180
    -V T T F D A E Y C R H G T C E R S E V G
      * Q L L M L S T V D M V H A K G Q K * V
      NNF * C * V L * T W Y M R K V R S R Y
9181 - ATTTGCCTATCTACCAGTGGTAGATGGGTTCTTAATAATGAGCATTACAGAGCTCTATCA - 9240
    -ICLSTSGRWVLNNEHYRALS
     FAYLPVVDGFLIMSITELYQ
       L P I Y Q W * M G S * * * A L Q S S I R
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9241 - GGAGTTTTCTGTGGTGTTGATGCGATGAATCTCATAGCTAACATCTTTACTCCTCTTGTG - 9300
   -GVFCGVDAMNLIANIFTPLV
   - E F S V V L M R * I S * L T S L L L C
     S F L W C * C D E S H S * H L Y S S C A
9301 - CAACCTGTGGGTGCTTTAGATGTGTCTGCTTCAGTAGTGGCTGGTGGTATTATTGCCATA - 9360
   -QPVGALDVSASVVAGGIIAI
   - N L W V L * M C L L Q * W L V V L L P Y
     T C G C F R C V C F S S G W W Y Y C H I
9361 - TTGGTGACTTGTGCTGCCTACTACTTTATGAAATTCAGACGTGTTTTTGGTGAGTACAAC - 9420
   -LVTCAAYYFMKFRRVFGEYN
     W * L V L P T T L * N S D V F L V S T T
     G D L C C L L Y E I Q T C F W * V Q P
-HVVAANALLFLMSFTILCLV
     M L L L M H F C F * C L S L Y S V W Y
     C C C C * C T F V F D V F H Y T L S G T
9481 - CCAGCTTACAGCTTTCTGCCGGGAGTCTACTCAGTCTTTTACTTGTACTTGACATTCTAT - 9540
   - P A Y S F L P G V Y S V F Y L Y L T F Y
     Q L T A F C R E S T Q S F T C T * H S I
     SLQLSAGSLLSLLLVLDILF
9541 - TTCACCAATGATGTTTCATTCTTGGCTCACCTTCAATGGTTTGCCATGTTTTCTCCTATT - 9600
   -FTNDVSFLAHLQWFAMFSPI
     S P M M F H S W L T F N G L P C F L L L
    HQ * C F I L G S P S M V C H V F S Y C
9601 - GTGCCTTTTTGGATAACAGCAATCTATGTATTCTGTATTTCTCTGAAGCACTGCCATTGG - 9660
   -V P F W I T A I Y V F C I S L K H C H W
    C L F G * Q Q S M Y S V F L * S T A I G
    A F L D N S N L C I L Y F S E A L P L V
9661 - TTCTTTAACAACTATCTTAGGAAAAGAGTCATGTTTAATGGAGTTACATTTAGTACCTTC - 9720
   -FFNNYLRKRVMFNGVTFSTF
     S L T T I L G K E S C L M E L H L V P S
     L * Q L S * E K S H V * W S Y I * Y L R
9721 - GAGGAGGCTGCTTTGTGTACCTTTTTGCTCAACAAGGAAATGTACCTAAAATTGCGTAGC - 9780
   -EEAALCTFLLNKEMYLKLRS
    R R L L C V P F C S T R K C T * N C V A
      G G C F V Y L F A Q Q G N V P K I A * R
9781 - GAGACACTGTTGCCACTTACACAGTATAACAGGTATCTTGCTCTATATAACAAGTACAAG - 9840
   -ETLLPLTQYNRYLALYNKYK
     R H C C H L H S I T G I L L Y I T S T S
      9841 - TATTTCAGTGGAGCCTTAGATACTACCAGCTATCGTGAAGCAGCTTGCTGCCACTTAGCA - 9900
   - Y F S G A L D T T S Y R E A A C C H L A
     ISVEP*ILPAIVKQLAAT*Q
      F Q W S L R Y Y Q L S * S S L L P L S K
-KALNDFSNSGADVLYQPPQT
     RL * M T L A T Q V L M F S T N H H R H
      G S K * L * Q L R C * C S L P T T T D I
9961 - TCAATCACTTCTGCTGTTCTGCAGAGTGGTTTTAGGAAAATGGCATTCCCGTCAGGCAAA - 10020
    -SITSAVLQSGFRKMAFPSGK
     Q S L L L F C R V V L G K W H S R Q A K
     N H F C C S A E W F * E N G I P V R Q S
10021 - GTTGAAGGGTGCATGGTACAAGTAACCTGTGGAACTACAACTCTTAATGGATTGTGGTTG - 10080
    -VEGCMVQVTCGTTTLNGLWL
     LKGAWYK*PVELQLLMDCGW
      * R V H G T S N L W N Y N S * W I V V G
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10081 - GATGACACAGTATACTGTCCAAGACATGTCATTTGCACAGCAGAAGACATGCTTAATCCT - 10140
   - D D T V Y C P R H V I C T A E D M L N P
   - M T O Y T V Q D M S F A Q Q K T C L I L
      * H S I L S K T C H L H S R R H A * S *
10141 - AACTATGAAGATCTGCTCATTCGCAAATCCAACCATAGCTTTCTTGTTCAGGCTGGCAAT - 10200
   -NYEDLLIRKSNHSFLVQAGN
   - T M K I C S F A N P T I A F L F R L A M
     L * R S A H S Q I Q P * L S C S G W Q C
10201 - GTTCAACTTCGTGTTATTGGCCATTCTATGCAAAATTGTCTGCTTAGGCTTAAAGTTGAT - 10260
    -VQLRVIGHSMQNCLLRLKVD
     FNFVLLAILCKIVCLGLKLI
      STSCYWPFYAKLSA*A*S*Y
10261 - ACTTCTAACCCTAAGACACCCAAGTATAAATTTGTCCGTATCCAACCTGGTCAAACATTT - 10320
    -TSNPKTPKYKFVRIQPGQTF
     LLTLRHPSINLSVSNLVKHF
     F * P * D T Q V * I C P Y P T W S N I F
10321 - TCAGTTCTAGCATGCTACAATGGTTCACCATCTGGTGTTTATCAGTGTGCCATGAGACCT - 10380
    -SVLACYNGSPSGVYQCAMRP
     OF * HATMVHHLVFISVP * DL
      SSSMLQWFTIWCLSVCHET*
10381 - AATCATACCATTAAAGGTTCTTTCCTTAATGGATCATGTGGTAGTGTTGGTTTTAACATT - 10440
    -NHTIKGSFLNGSCGSVGFNI
    - I I P L K V L S L M D H V V V L V L T L
    - S Y H * R F F P * W I M W * C W F * H *
10441 - GATTATGATTGCGTGTCTTTCTGCTATATGCATCATATGGAGCTTCCAACAGGAGTACAC - 10500
    - D Y D C V S F C Y M H H M E L P T G V H
    - I M I A C L S A I C I I W S F Q Q E Y T
     L * L R V F L L Y A S Y G A S N R S T R
-AGTDLEGKFYGPFVDRQTAQ
    - L V L T * K V N S M V H L L T D K L H R
    - WY*LRR*ILWSIC*QTNCTG
10561 - GCTGCAGGTACAGACAACCATAACATTAAATGTTTTGGCATGGCTGTATGCTGCTGTT - 10620
    - A A G T D T T I T L N V L A W L Y A A V
     L Q V Q T Q P * H * M F W H G C M L L L
      CRYRHNHNIKCFGMAVCCCY
10621 - ATCAATGGTGATAGGTGGTTTCTTAATAGATTCACCACTACTTTGAATGACTTTAACCTT - 10680
    -INGDRWFLNRFTTTLNDFNL
    - S M V I G G F L I D S P L L * M T L T L
      Q W * * V V S * * I H H Y F E * L * P C
10681 - GTGGCAATGAAGTACAACTATGAACCTTTGACACAAGATCATGTTGACATATTGGGACCT - 10740
    -VAMKYNYEPLTQDHVDILGP
     W Q * S T T M N L * H K I M L T Y W D L
      G N E V Q L * T F D T R S C * H I G T S
10741 - CTTTCTGCTCAAACAGGAATTGCCGTCTTAGATATGTGTGCTGCTTTGAAAGAGCTGCTG - 10800
    -LSAQTGIAVLDMCAALKELL
    - F L L K Q E L P S * I C V L L * K S C C
      FCSNRNCRLRYVCCFERAAA
10801 - CAGAATGGTATGAATGGTCGTACTATCCTTGGTAGCACTATTTTAGAAGATGAGTTTACA - 10860
    -QNGMNGRTILGSTILEDEFT
    - R M V * M V V L S L V A L F * K M S L H
      EWYEWSYYPW*HYFRR*VYT
10861 - CCATTTGATGTTTAGACAATGCTCTGGTGTTACCTTCCAAGGTAAGTTCAAGAAAATT - 10920
    - P F D V V R Q C S G V T F Q G K F K K I
    - H L M L L D N A L V L P S K V S S R K L
      I * C C * T M L W C Y L P R * V Q E N C
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10921 - GTTAAGGGCACTCATCATTGGATGCTTTTAACTTTCTTGACATCACTATTGATTCTTGTT - 10980
    -V K G T H H W M L L T F L T S L L I L V
    - L R A L I I G C F * L S * H H Y * F L F
      * G H S S L D A F N F L D I T I D S C S
10981 - CAAAGTACACAGTGGTCACTGTTTTTCTTTGTTTACGAGAATGCTTTCTTGCCATTTACT - 11040
    -QSTQWSLFFFVYENAFLPFT
    - K V H S G H C F S L F T R M L S C H L L
      K Y T V V T V F L C L R E C F L A I Y S
11041 - CTTGGTATTATGGCAATTGCTGCATGTGCTATGCTGCTTGTTAAGCATAAGCACGCATTC - 11100
    - L G I M A I A A C A M L L V K H K H A F
     LVLWQLLHVLCCLLSISTHS
      W Y Y G N C C M C Y A A C * A * A R I L
11101 - TTGTGCTTGTTTCTGTTACCTTCTCTTGCAACAGTTGCTTACTTTAATATGGTCTACATG - 11160
    -LCLFLLPSLATVAYFNMVYM
     C A C F C Y L L L Q Q L L T L I W S T C
      V L V S V T F S C N S C L L * Y G L H A
11161 - CCTGCTAGCTGGGTGATGCGTATCATGACATGGCTTGAATTGGCTGACACTAGCTTGTCT - 11220
    - P A S W V M R I M T W L E L A D T S L S
    - L L A G * C V S * H G L N W L T L A C L
     C * L G D A Y H D M A * I G * H * L V W
11221 - GGTTATAGGCTTAAGGATTGTGTTATGTATGCTTCAGCTTTAGTTTTGCTTATTCTCATG - 11280
    -GYRLKDCVMYASALVLILM
    - VIGLRIVLCMLQL*FCLFS*
    - L * A * G L C Y V C F S F S F A Y S H D
11281 - ACAGCTCGCACTGTTTATGATGATGCTGCTAGACGTGTTTGGACACTGATGAATGTCATT - 11340
    -TARTVYDDAARRVWTLMNVI
      Q L A L F M M M L L D V F G H * * M S L
       S S H C L * * C C * T C L D T D E C H Y
11341 - ACACTTGTTTACAAAGTCTACTATGGTAATGCTTTAGATCAAGCTATTTCCATGTGGGCC - 11400
    -TLVYKVYYGNALDQAISMWA
    - H L F T K S T M V M L * I K L F P C G P
       TCLQSLLW*CFRSSYFHVGL
11401 - TTAGTTATTTCTGTAACCTCTAACTATTCTGGTGTCGTTACGACTATCATGTTTTTAGCT - 11460
    -LVISVTSNYSGVVTTIMFLA
      * L F L * P L T I L V S L R L S C F * L
     SYFCNL * LFWCRYDYHVFS *
11461 - AGAGCTATAGTGTTTGTGTGTGTTGAGTATTACCCATTGTTATTACTGGCAACACC - 11520
    -RAIVFVCVEYYPLLFITGNT
    - E L * C L C V L S I T H C Y L L A T P
      S Y S V C V C * V L P I V I Y Y W Q H L
11521 - TTACAGTGTATCATGCTTGTTTATTGTTTCTTAGGCTATTGTTGCTGCTGCTACTTTGGC - 11580
    -LQCIMLVYCFLGYCCCYFG
     Y S V S C L F I V S * A I V A A A T L A
       T V Y H A C L L F L R L L L L L L W P
11581 - CTTTTCTGTTTACTCAACCGTTACTTCAGGCTTACTCTTGGTGTTTATGACTACTTGGTC - 11640
    - L F C L L N R Y F R L T L G V Y D Y L V
      F S V Y S T V T S G L L L V F M T T W S
       FLFTQPLLQAYSWCL*LLGL
11641 - TCTACACAAGAATTTAGGTATATGAACTCCCAGGGGCTTTTGCCTCCTAAGAGTAGTATT - 11700
    -STQEFRYMNSQGLLPPKSSI
      L H K N L G I * T P R G F C L L R V V L
       Y T R I * V Y E L P G A F A S * E * Y *
11701 - GATGCTTTCAAGCTTAACATTAAGTTGTTGGGTATTGGAGGTAAACCATGTATCAAGGTT - 11760
     -DAFKLNIKLLGIGGKPCIKV
      MLSSLTLSCWVLEVNHVSRL
       C F Q A * H * V V G Y W R * T M Y Q G C
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11761 - GCTACTGTACAGTCTAAAATGTCTGACGTAAAGTGCACATCTGTGGTACTGCTCTCGGTT - 11820
    - A T V Q S K M S D V K C T S V V L L S V
    - L L Y S L K C L T * S A H L W Y C S R F
      YCTV*NV*RKVHICGTALGS
11821 - CTTCAACAACTTAGAGTAGAGTCATCTTCTAAATTGTGGGCACAATGTGTACAACTCCAC - 11880
    -LQQLRVESSSKLWAQCVQLH
    - F N N L E * S H L L N C G H N V Y N S T
       STT * SR V I F * I V G T M C T T P Q
11881 - AATGATATTCTTCTTGCAAAAGACACAACTGAAGCTTTCGAGAAGATGGTTTCTCTTTTG - 11940
    -NDILLAKDTTEAFEKMVSLL
    - M I F F L Q K T Q L K L S R R W F L F C
      * Y S S C K R H N * S F R E D G F S F V
11941 - TCTGTTTTGCTATCCATGCAGGGTGCTGTAGACATTAATAGGTTGTGCGAGGAAATGCTC - 12000
    -S V L L S M Q G A V D I N R L C E E M L
     L F C Y P C R V L * T L I G C A R K C S
       C F A I H A G C C R H * * V V R G N A R
12001 - GATAACCGTGCTACTCTTCAGGCTATTGCTTCAGAATTTAGTTCTTTACCATCATATGCC - 12060
    -DNRATLQAIASEFSSLPSYA
     I T V L L F R L L L Q N L V L Y H H M P
      * P C Y S S G Y C F R I * F F T I I C R
12061 - GCTTATGCCACTGCCCAGGAGGCCTATGAGCAGGCTGTAGCTAATGGTGATTCTGAAGTC - 12120
    -AYATAQEAYEQAVANGDSEV
      L M P L P R R P M S R L * L M V I L K S
      L C H C P G G L * A G C S * W * F * S R
12121 - GTTCTCAAAAAGTTAAAGAAATCTTTGAATGTGGCTAAATCTGAGTTTGACCGTGATGCT - 12180
    -V L K K L K K S L N V A K S E F D R D A
      S Q K V K E I F E C G * I * V * P * C C
12181 - GCCATGCAACGCAAGTTGGAAAAGATGGCAGATCAGGCTATGACCCAAATGTACAAACAG - 12240
    - A M Q R K L E K M A D Q A M T Q M Y K Q
- P C N A S W K R W Q I R L * P K C T N R
     HATQVGKDGRSGYDPNVQTG
12241 - GCAAGATCTGAGGACAAGAGGGCAAAAGTAACTAGTGCTATGCAAACAATGCTCTTCACT - 12300
    -ARSEDKRAKVTSAMQTMLFT
      Q D L R T R G Q K * L V L C K Q C S S L
       KI * G Q E G K S N * C Y A N N A L H Y
12301 - ATGCTTAGGAAGCTTGATAATGATGCACTTAACAACATTATCAACAATGCGCGTGATGGT - 12360
    - M L R K L D N D A L N N I I N N A R D G
    - C L G S L I M M H L T T L S T M R V M V
       A * E A * * * C T * Q H Y Q Q C A * W L
12361 - TGTGTTCCACTCAACATCATACCATTGACTACAGCAGCCCAAACTCATGGTTGTTCCCT - 12420
    -CVPLNIIPLTTAAKLMVVVP
    - V F H S T S Y H * L Q Q P N S W L L S L
       CSTQHHTIDYSSQTHGCCP*
12421 - GATTATGGTACCTACAAGAACACTTGTGATGGTAACACCTTTACATATGCATCTGCACTC - 12480
    - D Y G T Y K N T C D G N T F T Y A S A L
    - I M V P T R T L V M V T P L H M H L H S
      LWYLQEHL*W*HLYICICTL
12481 - TGGGAAATCCAGCAAGTTGTTGATGCGGATAGCAAGATTGTTCAACTTAGTGAAATTAAC - 12540
    -WEIQQVVDADSKIVQLSEIN
    - G K S S K L L M R I A R L F N L V K L T
      G N P A S C * C G * Q D C S T * * N * H
12541 - ATGGACAATTCACCAAATTTGGCTTGGCCTCTTATTGTTACAGCTCTAAGAGCCAACTCA - 12600
    - M D N S P N L A W P L I V T A L R A N S
    - WTIHQIWLGLLLLQL*EPTQ
       G Q F T K F G L A S Y C Y S S K S Q L S
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12601 - GCTGTTAAACTACAGAATAATGAACTGAGTCCAGTAGCACTACGACAGATGTCCTGTGCG - 12660
    - A V K L Q N N E L S P V A L R Q M S C A
    - L L N Y R I M N * V Q * H Y D R C P V R
      C * T T E * * T E S S S T T T D V L C G
12661 - GCTGGTACCACACAACAGCTTGTACTGATGACAATGCACTTGCCTACTATAACAATTCG - 12720
    - A G T T Q T A C T D D N A L A Y Y N N S
     LVPHKQLVLMTMHLPTITIR
      W Y H T N S L Y * * Q C T C L L * Q F E
12721 - AAGGGAGGTAGGTTTGTGCTGGCATTACTATCAGACCACCAAGATCTCAAATGGGCTAGA - 12780
    -KGGRFVLALLSDHQDLKWAR
     REVGLCWHYYQTTKISNGLD
      G R * V C A G I T I R P P R S Q M G * I
12781 - TTCCCTAAGAGTGATGGTACAGGTACAATTTACACAGAACTGGAACCACCTTGTAGGTTT - 12840
    - F P K S D G T G T I Y T E L E P P C R F
     S L R V M V Q V Q F T Q N W N H L V G L
      P * E * W Y R Y N L H R T G T T L * V C
12841 - GTTACAGACACCAAAAGGGCCTAAAGTGAAATACTTGTACTTCATCAAAGGCTTAAAC - 12900
    -V T D T P K G P K V K Y L Y F I K G L N
     LQTHQKGLK*NTCTSSKA*T
      YRHTKRA*SEILVLHQRLKQ
12901 - AACCTAAATAGAGGTATGGTGCTGGGCAGTTTAGCTGCTACAGTACGTCTTCAGGCTGGA - 12960
    -NLNRGMVLGSLAATVRLQAG
     T * I E V W C W A V * L L Q Y V F R L E
      PK * RYGAGQFSCYSTSSGWK
12961 - AATGCTACAGAAGTACCTGCCAATTCAACTGTGCTTTCCTTCTGTGCTTTTGCAGTAGAC - 13020
    -NATEVPANSTVLSFCAFAVD
     M L Q K Y L P I Q L C F P S V L L Q * T
    - CYRSTCQFNCAFLLCFCSRP
13021 - CCTGCTAAAGCATATAAGGATTACCTAGCAAGTGGAGGACAACCAATCACCAACTGTGTG - 13080
    - P A K A Y K D Y L A S G G Q P I T N C V
- L L K H I R I T * Q V E D N Q S P T V *
       C * S I * G L P S K W R T T N H Q L C E
13081 - AAGATGTTGTGTACACACACTGGTACAGGACAGGCAATTACTGTAACACCAGAAGCTAAC - 13140
    - K M L C T H T G T G Q A I T V T P E A N
    - R C C V H T L V Q D R Q L L * H Q K L T
    - DVVYTHWYRTGNYCNTRS*H
13141 - ATGGACCAAGAGTCCTTTGGTGGTGCTTCATGTTGTCTGTATTGTAGATGCCACATTGAC - 13200
    - M D Q E S F G G A S C C L Y C R C H I D
- W T K S P L V V L H V V C I V D A T L T
       GPRVLWWCFMLSVL*MPH*P
- H P N P K G F C D L K G K Y V Q I P T T
       \verb|I Q I L K D S V T * K V S T S K Y L P L \\
       SKS*RIL*LER*VRPNTYHL
13261 - TGTGCTAATGACCCAGTGGGTTTTACACTTAGAAACACAGTCTGTACCGTCTGCGGAATG - 13320
    -CANDPVGFTLRNTVCTVCGM
    - V L M T Q W V L H L E T Q S V P S A E C
       C * * P S G F Y T * K H S L Y R L R N V
13321 - TGGAAAGGTTATGGCTGTAGTTGTGACCAACTCCGCGAACCCTTGATGCAGTCTGCGGAT - 13380
    -W K G Y G C S C D Q L R E P L M Q S A D
     ERLWL*L*PTPRTLDAVCGC
13381 - GCATCAACGTTTTTAAACGGGTTTGCGGTGTAAGTGCAGCCCGTCTTACACCGTGCGGCA - 13440
    - A S T F L N G F A V * V Q P V L H R A A
    - H Q R F * T G L R C K C S P S Y T V R H
       I N V F K R V C G V S A A R L T P C G T
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13441 - CAGGCACTAGTACTGATGTCGTCTACAGGGCTTTTGATATTTACAACGAAAAAAGTGCTG - 13500
    -QALVLMSSTGLLIFTTKKVL
    - R H * Y * C R L Q G F * Y L Q R K K C W
     G T S T D V V Y R A F D I Y N E K S A G
13501 - GTTTTGCAAAGTTCCTAAAAACTAATTGCTGTCGCTTCCAGGAGAAGGATGAGGAAGGCA - 13560
    -VLQSS*KLIAVASRRMRKA
    - F C K V P K N * L L S L P G E G * G R Q
      FAKFLKTNCCRFQEKDEEGN
13561 - ATTTATTAGACTCTTACTTTGTAGTTAAGAGGCATACTATGTCTAACTACCAACATGAAG - 13620
    -IY*TLTL*LRGILCLTINMK
     FIRLLLCS*EAYYV*LPT*R
      L L D S Y F V V K R H T M S N Y Q H E E
13621 - AGACTATTTATAACTTGGTTAAAGATTGTCCAGCGGTTGCTGTCCATGACTTTTTCAAGT - 13680
    -RLFITWLKIVQRLLSMTFSS
     DYL*LG*RLSSGCCP*LFQV
      TIYNLVKDCPAVAVHDFFKF
-LE * M V T W Y H I Y H V S V * L N T Q
     * S R W * H G T T Y I T S A S N * I H N
     RVDGDMVPHISRQRLTKYTM
13741 - TGGCTGATTTAGTCTATGCTCTACGTCATTTTGATGAGGGTAATTGTGATACATTAAAAG - 13800
    -W L I * S M L Y V I L M R V I V I H * K
     G * F S L C S T S F * * G * L * Y I K R
       ADLVYALRHFDEGNCDTLKE
13801 - AAATACTCGTCACATACAATTGCTGTGATGATGATTATTTCAATAAGAAGGATTGGTATG - 13860
    -KYSSHTIAVMMIISIRRIGM
    - N T R H I Q L L * * * L F Q * E G L V *
       I L V T Y N C C D D D Y F N K K D W Y D
13861 - ACTTCGTAGAGAATCCTGACATCTTACGCGTATATGCTAACTTAGGTGAGCGTGTACGCC - 13920
    - T S * R I L T S Y A Y M L T * V S V Y A
- L R R E S * H L T R I C * L R * A C T P
      F V E N P D I L R V Y A N L G E R V R Q
13921 - AATCATTATTAAAGACTGTACAATTCTGCGATGCTATGCGTGATGCAGGCATTGTAGGCG - 13980
    -NHY*RLYNSAMLCVMQAL*A
-IIIKDCTILRCYA*CRHCRR
      S L L K T V Q F C D A M R D A G I V G V
13981 - TACTGACATTAGATAATCAGGATCTTAATGGGAACTGGTACGATTTCGGTGATTTCGTAC - 14040
    - Y * H * I I R I L M G T G T I S V I S Y
    - T D I R * S G S * W E L V R F R * F R T
      L T L D N Q D L N G N W Y D F G D F V Q
14041 - AAGTAGCACCAGGCTGCGGAGTTCCTATTGTGGATTCATATTACTCATTGCTGATGCCCA - 14100
    -K * H Q A A E F L L W I H I T H C * C P
      S S T R L R S S Y C G F I L L I A D A H
       V A P G C G V P I V D S Y Y S L L M P I
14101 - TCCTCACTTTGACTAGGGCATTGGCTGCTGAGTCCCATATGGATGCTGATCTCGCAAAAC - 14160
    -SSL * L G H W L L S P I W M L I S Q N
     P H F D * G I G C * V P Y G C * S R K T
       L T L T R A L A A E S H M D A D L A K P
14161 - CACTTATTAAGTGGGATTTGCTGAAATATGATTTTACGGAAGAGAGACTTTGTCTCTTCG - 14220
    - H L L S G I C * N M I L R K R D F V S S
      T Y * V G F A E I * F Y G R E T L S L R
       LIKWDLLKYDFTEERLCLFD
14221 - ACCGTTATTTTAAATATTGGGACCAGACATACCATCCCAATTGTATTAACTGTTTGGATG - 14280 ·
    -TVILNIGTRHTIPIVLTVWM
    - P L F * I L G P D I P S Q L Y * L F G *
       R Y F K Y W D Q T Y H P N C I N C L D D
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14281 - ATAGGTGTATCCTTCATTGTGCAAACTTTAATGTGTTATTTTCTACTGTGTTTCCACCTA - 14340
    -IGVSFIVQTLMCYFLLCFHL
    - * V Y P S L C K L * C V I F Y C V S T Y
- R C I L H C A N F N V L F S T V F P P T
14341 - CAAGTTTTGGACCACTAGTAAGAAAATATTTGTAGATGGTGTTCCTTTTGTTGTTCAA - 14400
    -QVLDH**EKYL*MVFLLLFQ
    K F W T T S K K N I C R W C S F C C F N
      SFGPLVRKIFVDGVPFVVST
14401 - CTGGATACCATTTTCGTGAGTTAGGAGTCGTACATAATCAGGATGTAAACTTACATAGCT - 14460
    -LDTIFVS*ESYIIRM*TYIA
     WIPFS * VRSRT * SGCKLT * L
      G Y H F R E L G V V H N Q D V N L H S S
-RVSVSRNF * CMLLIQLCMQL
     A S Q F Q G T F S V C C * S S Y A C S F
      R L S F K E L L V Y A A D P A M H A A S
-LAIYC * INALHAFQ * LH * Q T
     W Q F I A R * T H Y M L F S S C T N K Q
      G N L L L D K R T T C F S V A A L T N N
14581 - ATGTTGCTTTTCAAACTGTCAAACCCGGTAATTTTAATAAAGACTTTTATGACTTTGCTG - 14640
    -M L L F K L S N P V I L I K T F M T L L
     C C F S N C Q T R * F * * R L L * L C C
      V A F Q T V K P G N F N K D F Y D F A V
14641 - TGTCTAAAGGTTTCTTTAAGGAAGGAAGTTCTGTTGAACTAAAACACTTCTTTGCTC - 14700
    -CLKVSLRKEVLLN*NTSSLL
     V * R F L * G R K F C * T K T L L C S
      S K G F F K E G S S V E L K H F F F A Q
14701 - AGGATGGCAACGCTGCTATCAGTGATTATGACTATTATCGTTATAATCTGCCAACAATGT - 14760
    -RMATLLSVIMTIIVIICQQC
    - G W Q R C Y Q * L * L L S L * S A N N V
      D G N A A I S D Y D Y Y R Y N L P T M C
14761 - GTGATATCAGACAACTCCTATTCGTAGTTGAAGTTGTTGATAAATACTTTGATTGTTACG - 14820
    -VISDNSYS * LKLLINTLIVT
       Y Q T T P I R S * S C * * I L * L L R
      D I R Q L L F V V E V V D K Y F D C Y D
14821 - ATGGTGGCTGTATTAATGCCAACCAAGTAATCGTTAACAATCTGGATAAATCAGCTGGTT - 14880
    -MVAVLMPTK*SLTIWINQLV
    - W W L Y * C Q P S N R * Q S G * I S W F
       G G C I N A N Q V I V N N L D K S A G F
14881 - TCCCATTTAATAAATGGGGTAAGGCTAGACTTTATTATGACTCAATGAGTTATGAGGATC - 14940
    -SHLINGVRLDFIMTQ * VMRI
      PI * * M G * G * T L L * L N E L * G S
       P F N K W G K A R L Y Y D S M S Y E D Q
14941 - AAGATGCACTTTTCGCGTATACTAAGCGTAATGTCATCCCTACTATAACTCAAATGAATC - 15000
    - K M H F S R I L S V M S S L L * L K * I
      R C T F R V Y * A * C H P Y Y N S N E S
       DALFAYTKRNVIPTITQMNL
15001 - TTAAGTATGCCATTAGTGCAAAGAATAGAGCTCGCACCGTAGCTGGTGTCTCTATCTGTA - 15060
    -LSMPLVQRIELAP*LVSLSV
       * V C H * C K E * S S H R S W C L Y L *
      K Y A I S A K N R A R T V A G V S I C S
15061 - GTACTATGACAAATAGACAGTTTCATCAGAAATTATTGAAGTCAATAGCCGCCACTAGAG - 15120
    -VL * Q I D S F I R N Y * S Q * P P L E
      Y Y D K * T V S S E I I E V N S R H * R
       TMTNRQFHQKLLKSIAATRG
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-ELLW * LEQASFTVAGIIC * K
    - SYCGNWNKQVLRWLA * YVKN
      A T V V I G T S K F Y G G W H N M L K T
15181 - CTGTTTACAGTGATGTAGAAACTCCACACCTTATGGGTTGGGATTATCCAAAATGTGACA - 15240
    -LFTVM*KLHTLWVGIIQNVT
    CLQ * CRNSTPYGLGLSKM * Q
      V Y S D V E T P H L M G W D Y P K C D R
15241 - GAGCCATGCCTAACATGCTTAGGATAATGGCCTCTCTTGTTCTTGCTCGCAAACATAACA - 15300
    -EPCLTCLG * WPLLFLLANIT
     S H A * H A * D N G L S C S Q T * H
      AMPNMLRIMASLVLARKHNT
15301 - CTTGCTGTAACTTATCACACCGTTTCTACAGGTTAGCTAACGAGTGTGCGCAAGTATTAA - 15360
    -LAVTYHTVSTG*LTSVRKY*
     LL*LITPFLQVS*RVCASIK
      C C N L S H R F Y R L A N E C A Q V L S
15361 - GTGAGATGGTCATGTGGCGGCTCACTATATGTTAAACCAGGTGGAACATCATCCGGTG - 15420
    -VRWSCVAAHYMLNQVEHHPV
     * D G H V W R L T I C * T R W N I I R *
      E M V M C G G S L Y V K P G G T S S G D
15421 - ATGCTACAACTGCTTATGCTAATAGTGTCTTTAACATTTGTCAAGCTGTTACAGCCAATG - 15480
    -MLQLLMLIVSLTFVKLLQPM
     C Y N C L C * * C L * H L S S C Y S Q C
      A T T A Y A N S V F N I C Q A V T A N V
15481 - TAAATGCACTTCTTTCAACTGATGGTAATAAGATAGCTGACAAGTATGTCCGCAATCTAC - 15540
    - * M H F F Q L M V I R * L T S M S A I Y
- K C T S F N * W * * D S * Q V C P Q S T
      NALLSTDGNKIADKYVRNLQ
15541 - AACACAGGCTCTATGAGTGTCTCTATAGAAATAGGGATGTTGATCATGAATTCGTGGATG - 15600
    -NTGSMSVSIEIGMLIMNSWM
      T Q A L * V S L * K * G C * S * I R G *
      HRLYECLYRNRDVDHEFVDE
15601 - AGTTTTACGCTTACCTGCGTAAACATTTCTCCATGATGATTCTTCTGATGATGCCGTTG - 15660
    -SFTLTCVNISP**FFLMMPL
    - V L R L P A * T F L H D D S F * * C R C
      F Y A Y L R K H F S M M I L S D D A V V
15661 - TGTGCTATAACAGTAACTATGCGGCTCAAGGTTTAGTAGCATTAAGAACTTTAAGG - 15720
    -CAITVTMRLKV**LALRTLR
    - V L * Q * L C G S R F S S * H * E L * G
       C Y N S N Y A A Q G L V A S I K N F K A
15721 - CAGTTCTTTATTATCAAAATAATGTGTTCATGTCTGAGGCAAAATGTTGGACTGAGACTG - 15780
    -QFFIIKIMCSCLRQNVGLRL
      SSLLSK * CVHV * GKMLD * D *
       \begin{smallmatrix} V&L&Y&Y&Q&N&N&V&F&M&S&E&A&K&C&W&T&E&T&D\end{smallmatrix}
15781 - ACCTTACTAAAGGACCTCACGAATTTTGCTCACAGCATACAATGCTAGTTAAACAAGGAG - 15840
    -TLLKDLTNFAHSIQC*LNKE
-PY*RTSRILLTAYNAS*TRR
       L T K G P H E F C S Q H T M L V K Q G D
15841 - ATGATTACGTGTACCTGCCTTACCCAGATCCATCAAGAATATTAGGCGCAGGCTGTTTTG - 15900
    - M I T C T C L T Q I H Q E Y * A Q A V L
      * LRVPALPRSIKNIRRRLFC
      D Y V Y L P Y P D P S R I L G A G C F V
15901 - TCGATGATATTGTCAAAACAGATGGTACACTTATGATTGAAAGGTTCGTGTCACTGGCTA - 15960
    -SMILSKQMVHL * LKGSCHW L
      R * Y C Q N R W Y T Y D * K V R V T G Y
       D D I V K T D G T L M I E R F V S L A I
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15961 - TTGATGCTTACCCACTTACAAAACATCCTAATCAGGAGTATGCTGATGTCTTTCACTTGT - 16020
    -L M L T H L Q N I L I R S M L M S F T C
    - * C L P T Y K T S * S G V C * C L S L V
      D A Y P L T K H P N Q E Y A D V F H L Y
16021 - ATTTACAATACATTAGAAAGTTACATGATGAGCTTACTGGCCACATGTTGGACATGTATT - 16080
    -IYNTLESYMMSLLATCWTCI
    - F T I H * K V T * * A Y W P H V G H V F
      LQYIRKLHDELTGHMLDMYS
16081 - CCGTAATGCTAACTAATGATAACACCTCACGGTACTGGGAACCTGAGTTTTATGAGGCTA - 16140
    -P * C * L M I T P H G T G N L S F M R L
     R N A N * * * H L T V L G T * V L * G Y
      V M L T N D N T S R Y W E P E F Y E A M
16141 - TGTACACACCACATACAGTCTTGCAGGCTGTAGGTGCTTGTGTATTGTGCAATTCACAGA - 16200
    -CTHHIQSCRL*VLVYCAIHR
      V H T T Y S L A G C R C L C I V Q F T D
       Y T P H T V L Q A V G A C V L C N S Q T
16201 - CTTCACTTCGTTGCGGTGCCTGTATTAGGAGACCATTCCTATGTTGCAAGTGCTGCTATG - 16260
    - L H F V A V P V L G D H S Y V A S A A M
      FTSLRCLY*ETIPMLQVLL*
       S L R C G A C I R R P F L C C K C C Y D
16261 - ACCATGTCATTTCAACATCACACAAATTAGTGTTGTCTGTTAATCCCTATGTTTGCAATG - 16320
    -TMSFQHHTN*CCLLIPMFAM
    - PCHFNITQISVVC*SLCLQC
- HVISTSHKLVLSVNPYVCNA
16321 - CCCCAGGTTGTGATGTCACTGATGTGACACAACTGTATCTAGGAGGTATGAGCTATTATT - 16380
    - P Q V V M S L M * H N C I * E V * A I I
    - PRL * CH * CDTTVSRRYELLL
       P G C D V T D V T Q L Y L G G M S Y Y C
16381 - GCAAGTCACATAAGCCTCCCATTAGTTTTCCATTATGTGCTAATGGTCAGGTTTTTGGTT - 16440
    - A S H I S L P L V F H Y V L M V R F L V
- Q V T * A S H * F S I M C * W S G F W F
       K S H K P P I S F P L C A N G Q V F G L
16441 - TATACAAAAACACATGTGTAGGCAGTGACAATGTCACTGACTTCAATGCGATAGCAACAT - 16500
    - Y T K T H V * A V T M S L T S M R * Q H
      I Q K H M C R Q * Q C H * L Q C D S N M
       Y K N T C V G S D N V T D F N A I A T C
16501 - GTGATTGGACTAATGCTGGCGATTACATACTTGCCAACACTTGTACTGAGAGACTCAAGC - 16560
    -VIGLMLAITYLPTLVLRDSS
      * L D * C W R L H T C Q H L Y * E T Q A
      DWTNAGDYILANTCTERLKL
16561 - TTTTCGCAGCAGAAACGCTCAAAGCCACTGAGGAAACATTTAAGCTGTCATATGGTATTG - 16620
     -FSQQKRSKPLRKHLSCHMVL
      FRSRNAQSH*GNI*AVIWYC
       F A A E T L K A T E E T F K L S Y G I A
16621 - CCACTGTACGCGAAGTACTCTCTGACAGAGAATTGCATCTTTCATGGGAGGTTGGAAAAC - 16680
     - P L Y A K Y S L T E N C I F H G R L E N
      HCTRSTL*QRIASFMGGWKT
       T V R E V L S D R E L H L S W E V G K P
16681 - CTAGACCACCATTGAACAGAAACTATGTCTTTACTGGTTACCGTGTAACTAAAAATAGTA - 16740
     -LDHH*TETMSLLVTV*LKIV
      * T T I E Q K L C L Y W L P C N * K * *
       R P P L N R N Y V F T G Y R V T K N S K
16741 - AAGTACAGATTGGAGAGTACACCTTTGAAAAAGGTGACTATGGTGATGCTGTTGTGTACA - 16800
     -KYRLESTPLKKVTMVMLLCT
      STDWRVHL*KR*LW*CCCVQ
       V Q I G E Y T F E K G D Y G D A V V Y R
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16801 - GAGGTACTACGACATACAAGTTGAATGTTGGTGATTACTTTGTGTTGACATCTCACACTG - 16860
    -EVLRHTS * MLVITLC * HLTL
    - R Y Y D I Q V E C W * L L C V D I S H C
       G T T T Y K L N V G D Y F V L T S H T V
16861 - TAATGCCACTTAGTGCACCTACTCTAGTGCCACAAGAGCACTATGTGAGAATTACTGGCT - 16920
    - * C H L V H L L * C H K S T M * E L L A
    - N A T * C T Y S S A T R A L C E N Y W L
       M P L S A P T L V P Q E H Y V R I T G L
16921 - TGTACCCAACACTCAACATCTCAGATGAGTTTTCTAGCAATGTTGCAAATTATCAAAAGG - 16980
    -CTQHSTSQMSFLAMLQIIKR
      V P N T Q H L R * V F * Q C C K L S K G
       Y P T L N I S D E F S S N V A N Y Q K V
16981 - TCGGCATGCAAAAGTACTCTACACTCCAAGGACCACCTGGTACTGGTAAGAGTCATTTTG - 17040
    -SACKSTLHSKDHLVLVRVIL
     R H A K V L Y T P R T T W Y W * E S F C
      G M Q K Y S T L Q G P P G T G K S H F A
17041 - CCATCGGACTTGCTCTATTACCCATCTGCTCGCATAGTGTATACGGCATGCTCTCATG - 17100
     -PSDLLSITHLLA*CIRHALM
     H R T C S L L P I C S H S V Y G M L S C
      I G L A L Y Y P S A R I V Y T A C S H A
17101 - CAGCTGTTGATGCCCTATGTGAAAAGGCATTAAAATATTTGCCCATAGATAAATGTAGTA - 17160
    -Q L L M P Y V K R H * N I C P * I N V V
      SC * C P M * K G I K I F A H R * M * *
      AVDALCEKALKYLPIDKCSR
17161 - GAATCATACCTGCGCGTGCGCGCGTAGAGTGTTTTGATAAATTCAAAGTGAATTCAACAC - 17220
    -ESYLRVRA*SVLINSK*IQH
     - N H T C A C A R R V F * * I Q S E F N T
       I I P A R A R V E C F D K F K V N S T L
17221 - TAGAACAGTATGTTTTCTGCACTGTAAATGCATTGCCAGAAACAACTGCTGACATTGTAG - 17280
     -* N S M F S A L * M H C Q K Q L L T L *
     - R T V C F L H C K C I A R N N C * H C S
       EQYVFCTVNALPETTADIVV
17281 - TCTTTGATGAAATCTCTATGGCTACTAATTATGACTTGAGTGTTGTCAATGCTAGACTTC - 17340
     -SLMKSLWLLIMT * VLSMLD F
      L * * N L Y G Y * L * L E C C Q C * T S
        F D E I S M A T N Y D L S V V N A R L R
17341 - GTGCAAAACACTACGTCTATATTGGCGATCCTGCTCAATTACCAGCCCCCGCACATTGC - 17400
     -V Q N T T S I L A I L N Y Q P P A H C
       C K T L R L Y W R S C S I T S P P H I A
        A K H Y V Y I G D P A Q L P A P R T L L
17401 - TGACTAAAGGCACACTAGAACCAGAATATTTTAATTCAGTGTGCAGACTTATGAAAACAA - 17460
     - * L K A H * N Q N I L I Q C A D L * K Q
      D * R H T R T R I F * F S V Q T Y E N N
        TKGTLEPEYFNSVCRLMKTI
 17461 - TAGGTCCAGACATGTTCCTTGGAACTTGTCGCCGTTGTCCTGCTGAAATTGTTGACACTG - 17520
     - * V Q T C S L E L V A V V L L K L L T L
- R S R H V P W N L S P L S C * N C * H C
        G P D M F L G T C R R C P A E I V D T V
 17521 - TGAGTGCTTTAGTTTATGACAATAAGCTAAAAGCACACAAGGATAAGTCAGCTCAATGCT - 17580
     - * V L * F M T I S * K H T R I S Q L N A
       E C F S L * Q * A K S T Q G * V S S M L
        S A L V Y D N K L K A H K D K S A Q C F
 17581 - TCAAAATGTTCTACAAAGGTGTTATTACACATGATGTTTCATCTGCAATCAACAGACCTC - 17640
     -SKCSTKVLLHMMFHLQSTDL
       Q N V L Q R C Y Y T * C F I C N Q Q T S
        K M F Y K G V I T H D V S S A I N R P Q
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17641 - AAATAGGCGTTGTAAGAGAATTTCTTACACGCAATCCTGCTTGGAGAAAAGCTGTTTTTA - 17700
    -K * A L * E N F L H A I L L G E K L F L
    - N R R C K R I S Y T Q S C L E K S C F Y
     I G V V R E F L T R N P A W R K A V F I
17701 - TCTCACCTTATAATTCACAGAACGCTGTAGCTTCAAAAATCTTAGGATTGCCTACGCAGA - 17760
    -SHLIIHRTL*LQKS*DCLRR
    - L T L * F T E R C S F K N L R I A Y A D
      S P Y N S Q N A V A S K I L G L P T Q T
17761 - CTGTTGATTCATCACAGGGTTCTGAATATGACTATGTCATATTCACACAAACTACTGAAA - 17820
    -LLIHHRVLNMTMSYSHKLLK
       * F I T G F * I * L C H I H T N Y * N
      V D S S Q G S E Y D Y V I F T Q T T E T
17821 - CAGCACACTCTTGTAATGTCAACCGCTTCAATGTGGCTATCACAAGGGCAAAAATTGGCA - 17880
    -QHTLVMSTASMWLSQGQKLA
      STLL * C Q P L Q C G Y H K G K N W H
      A H S C N V N R F N V A I T R A K I G I
17881 - TTTTGTGCATAATGTCTGATAGAGATCTTTATGACAAACTGCAATTTACAAGTCTAGAAA - 17940
    -FCA * CLIEIFM TNCNLQ V * K
     F V H N V * * R S L * Q T A I Y K S R N
     LCIMSDRDLYDKLQFTSLEI
17941 - TACCACGTCGCAATGTGGCTACATTACAAGCAGAAAATGTAACTGGACTTTTTAAGGACT - 18000
    - Y H V A M W L H Y K Q K M * L D F L R T
    - T T S Q C G Y I T S R K C N W T F * G L
    - PRRNVATLQAENVTGLFKDC
18001 - GTAGTAAGATCATTACTGGTCTTCATCCTACACAGGCACCTACACACCTCAGCGTTGATA - 18060
    -VVRSLLVFILHRHLHTSALI
      * * D H Y W S S S Y T G T Y T P Q R * Y
       S K I I T G L H P T Q A P T H L S V D I
18061 - TAAAATTCAAGACTGAAGGATTATGTGTTGACATACCAGGCATACCAAAGGACATGACCT - 18120
    - * N S R L K D Y V L T Y Q A Y Q R T * P
- K I Q D * R I M C * H T R H T K G H D L
       K F K T E G L C V D I P G I P K D M T Y
18121 - ACCGTAGACTCATCTCTATGATGGGTTTCAAAATGAATTACCAAGTCAATGGTTACCCTA - 18180
    -TVDSSL*WVSK*ITKSMVTL
    - P * T H L Y D G F Q N E L P S Q W L P *
      R R L I S M M G F K M N Y Q V N G Y P N
-ICLSPAKKLFVTFVRGLALM
    - Y V Y H P R R S Y S S R S C V D W L * C
      M F I T R E E A I R H V R A W I G F D V
-* R A V M Q L E M L W V L T Y L S S * D
    - R G L S C N * R C C G Y * P T S P A R I
      E G C H A T R D A V G T N L P L Q L G F
18301 - TTTCTACAGGTGTTAACTTAGTAGCTGTACCGACTGGTTATGTTGACACTGAAAATAACA - 18360
    -FLQVLT**LYRLVMLTLKIT
      FYRC*LSSCTDWLC*H*K*H
       S T G V N L V A V P T G Y V D T E N N T
18361 - CAGAATTCACCAGAGTTAATGCAAAACCTCCACCAGGTGACCAGTTTAAACATCTTATAC - 18420
    -QNSPELMQNLHQVTSLNILY
      R I H Q S * C K T S T R * P V * T S Y T
      E F T R V N A K P P P G D Q F K H L I P
18421 - CACTCATGTATAAAGGCTTGCCCTGGAATGTAGTGCGTATTAAGATAGTACAAATGCTCA - 18480
    - H S C I K A C P G M * C V L R * Y K C S
    - T H V * R L A L E C S A Y * D S T N A Q
       L M Y K G L P W N V V R I K I V Q M L S
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18481 - GTGATACACTGAAAGGATTGTCAGACAGAGTCGTGTTCGTCCTTTGGGCGCATGGCTTTG - 18540
    -VIH * K D C Q T E S C S S F G R M A L
    - * Y T E R I V R Q S R V R P L G A W L *
      DTLKGLSDRVVFVLWAHGFE
18541 - AGCTTACATCAATGAAGTACTTTGTCAAGATTGGACCTGAAAGAACGTGTTGTCTGTGTG - 18600
    -SLHQ*STLSRLDLKERVVCV
    - A Y I N E V L C Q D W T * K N V L S V *
      LTSMKYFVKIGPERTCCLCD
18601 - ACAAACGTGCAACTTGCTTTTCTACTTCATCAGATACTTATGCCTGGAATCATTCTG - 18660
    -TNVQLAFLLHQILMPAGIIL
     Q T C N L L F Y F I R Y L C L L E S F C
      K R A T C F S T S S D T Y A C W N H S V
18661 - TGGGTTTTGACTATGTCTATAACCCATTTATGATTGATGTTCAGCAGTGGGGCTTTACGG - 18720
    -W V L T M S I T H L * L M F S S G A L R
      G F * L C L * P I Y D * C S A V G L Y G
      G F D Y V Y N P F M I D V Q Q W G F T G
18721 - GTAACCTTCAGAGTAACCATGACCAACATTGCCAGGTACATGGAAATGCACATGTGGCTA - 18780
    -V T F R V T M T N I A R Y M E M H M W L
      * P S E * P * P T L P G T W K C T C G *
      N L Q S N H D Q H C Q V H G N A H V A S
18781 - GTTGTGATGCTATCATGACTAGATGTTTAGCAGTCCATGAGTGCTTTGTTAAGCGCGTTG - 18840
    -VVMLS*LDV*QSMSALLSAL
    - L * C Y H D * M F S S P * V L C * A R *
      CDAIMTRCLAVHECFVKRVD
18841 - ATTGGTCTGTTGAATACCCTATTATAGGAGATGAACTGAGGGTTAATTCTGCTTGCAGAA - 18900
    -IGLLNTLL*EMN*GLILLAE
    - L V C * I P Y Y R R * T E G * F C L Q K
      W S V E Y P I I G D E L R V N S A C R K
18901 - AAGTACAACACATGGTTGTGAAGTCTGCATTGCTTGATAAGTTTCCAGTTCTTCATG - 18960
    -KYNTWL*SLHCLLISFQFFM
-STTHGCEVCIAC**VSSSS*
       V Q H M V V K S A L L A D K F P V L H D
18961 - ACATTGGAAATCCAAAGGCTATCAAGTGTGTGCCTCAGGCTGAAGTAGAATGGAAGTTCT - 19020
    -TLEIQRLSSVCLRLK*NGSS
    - H W K S K G Y Q V C A S G * S R M E V L
       I G N P K A I K C V P Q A E V E W K F Y
19021 - ACGATGCTCAGCCATGTAGTGACAAAGCTTACAAAATAGAGGAACTCTTCTATTCTTATG - 19080
    -TMLSHVVTKLTK*RNSSILM
     R C S A M * * Q S L Q N R G T L L F L C
       D A Q P C S D K A Y K I E E L F Y S Y A
19081 - CTACACATCACGATAAATTCACTGATGGTGTTTGTTTTGGAATTGTAACGTTGATC - 19140
    -L H I T I N S L M V F V C F G I V T L I
      YTSR*IH*WCLFVLEL*R*S
       T H H D K F T D G V C L F W N C N V D R
19141 - GTTACCCAGCCAATGCAATTGTGTGTGTGGGTTTGACACAAGAGTCTTGTCAAACTTGAACT - 19200
    -V T Q P M Q L C V G L T Q E S C Q T * T
      L P S Q C N C V * V * H K S L V K L E L
       Y P A N A I V C R F D T R V L S N L N L
- Y Q A V M V V C M * I S M H S T L Q L
      TRL*WW*FVCE*ACIPHSSF
       P G C D G G S L Y V N K H A F H T P A F
-SIKVHLLI*SNCLSFTILIV
      R * K C I Y * F K A I A F L L F * * S
       D K S A F T N L K Q L P F F Y Y S D S P
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19321 - CTTGTGAGTCTCATGGCAAACAAGTAGTGTCGGATATTGATTATGTTCCACTCAAATCTG - 19380
    -LVSLMANK * CRILIMFHSNL
    C E S H G K Q V V S D I D Y V P L K S A
19381 - CTACGTGTATTACACGATGCAATTTAGGTGGTGCTGTTTGCAGACACCATGCAAATGAGT - 19440
    -LRVLHDAI*VVLFADTMQMS
    - Y V Y Y T M Q F R W C C L Q T P C K * V
      T C I T R C N L G G A V C R H H A N E Y
19441 - ACCGACAGTACTTGGATGCATATAATATGATGATTTCTGCTGGATTTAGCCTATGGATTT - 19500
    -TDSTWMHII**FLLDLAYGF
     PTVLGCI*YDDFCWI*PMDL
      R Q Y L D A Y N M M I S A G F S L W I Y
19501 - ACAAACAATTTGATACTTATAACCTGTGGAATACATTTACCAGGTTACAGAGTTTAGAAA - 19560
    -TNNLILITCGIHLPGYRV * K
      Q T I * Y L * P V E Y I Y Q V T E F R K
     KQFDTYNLWNTFTRLQSLEN
19561 - ATGTGGCTTATAATGTTGTTAATAAAGGACACTTTGATGGACACGCCGGCGAAGCACCTG - 19620
    - M W L I M L L I K D T L M D T P A K H L
    - C G L * C C * * R T L * W T R R S T C
      V A Y N V V N K G H F D G H A G E A P V
19621 - TTTCCATCATTAATAATGCTGTTTACACAAAGGTAGATGGTATTGATGTGGAGATCTTTG - 19680
    -FPSLIMLFTQR*MVLMWRSL
      F H H * * C C L H K G R W Y * C G D L *
       S I I N N A V Y T K V D G I D V E I F E
19681 - AAAATAAGACAACACTTCCTGTTAATGTTGCATTTGAGCTTTGGGCTAAGCGTAACATTA - 19740
    -KIRQHFLLMLHLSFGLSVTL
    - K * D N T S C * C C I * A L G * A * H *
      N K T T L P V N V A F E L W A K R N I K
19741 - AACCAGTGCCAGAGATTAAGATACTCAATAATTTGGGTGTTGATATCGCTGCTAATACTG - 19800
    -NQCQRLRYSIIWVLISLLIL
      TSARD * DTQ * FGC * YRC * YC
       P V P E I K I L N N L G V D I A A N T V
19801 - TAATCTGGGACTACAAAAGAGAAGCCCCAGCACATGTATCTACAATAGGTGTCTGCACAA - 19860
    - * S G T T K E K P Q H M Y L Q * V S A Q
    - N L G L Q K R S P S T C I Y N R C L H N
      I W D Y K R E A P A H V S T I G V C T M
19861 - TGACTGACATTGCCAAGAAACCTACTGAGAGTGCTTGTTCTTCACTTACTGTCTTGTTTG - 19920
    - * L T L P R N L L R V L V L H L L S C L
    - D * H C Q E T Y * E C L F F T Y C L V *
       T D I A K K P T E S A C S S L T V L F D
19921 - ATGGTAGAGTGGAAGGACAGGTAGACCTTTTTAGAAACGCCCGTAATGGTGTTTTAATAA - 19980
     - M V E W K D R * T F L E T P V M V F * *
      W * S G R T G R P F * K R P * W C F N N
       G R V E G Q V D L F R N A R N G V L I T
19981 - CAGAAGGTTCAGTCAAAGGTCTAACACCTTCAAAGGGACCAGCACAAGCTAGCGTCAATG - 20040
     -QKVQSKV*HLQRDQHKLASM
      R R F S Q R S N T F K G T S T S * R Q W
       E G S V K G L T P S K G P A Q A S V N G
20041 - GAGTCACATTAATTGGAGAATCAGTAAAAACACAGTTTAACTACTTTAAGAAAGTAGACG - 20100
     -ESH*LENQ*KHSLTTLRK*T
       S H I N W R I S K N T V * L L * E S R R
       V T L I G E S V K T Q F N Y F K K V D G
 20101 - GCATTATTCAACAGTTGCCTGAAACCTACTTTACTCAGAGCAGAGACTTAGAGGATTTTA - 20160
     -ALFNSCLKPTLLRAET*RIL
      H Y S T V A * N L L Y S E Q R L R G F *
       I I Q Q L P E T Y F T Q S R D L E D F K
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20161 - AGCCCAGATCACAAATGGAAACTGACTTTCTCGAGCTCGCTATGGATGAATTCATACAGC - 20220
    -SPDHKWKLTFSSSLWMNSYS
    - A Q I T N G N * L S R A R Y G * I H T A
     PRSQMETDFLELAMDEFIQR
20221 - GATATAAGCTCGAGGGCTATGCCTTCGAACACATCGTTTATGGAGATTTCAGTCATGGAC - 20280
    -DISSRAMPSNTSFMEISVMD
     I * A R G L C L R T H R L W R F Q S W T
      Y K L E G Y A F E H I V Y G D F S H G Q
20281 - AACTTGGCGGTCTTCATTTAATGATAGGCTTAGCCAAGCGCTCACAAGATTCACCACTTA - 20340
    -NLAVFI***A*PSAHKIHHL
      T W R S S F N D R L S Q A L T R F T T *
      L G G L H L M I G L A K R S Q D S P L K
20341 - AATTAGAGGATTTTATCCCTATGGACAGCACAGTGAAAAATTACTTCATAACAGATGCGC - 20400
    -N * R I L S L W T A Q * K I T S * Q M R
      I R G F Y P Y G Q H S E K L L H N R C A
       L E D F I P M D S T V K N Y F I T D A Q
20401 - AAACAGGTTCATCAAAATGTGTGTGTTCTGTGATTGATCTTTTACTTGATGACTTTGTCG - 20460
    -KQVHQNVCVL*LIFYLMTLS
    - N R F I K M C V F C D * S F T * * L C R
    - TGSSKCVCSVIDLLLDDFVE
20461 - AGATAATAAAGTCACAAGATTTGTCAGTGATTTCAAAAGTGGTCAAGGTTACAATTGACT - 20520
    -R * * S H K I C Q * F Q K W S R L Q L T
    - D N K V T R F V S D F K S G Q G Y N * L
       I I K S Q D L S V I S K V V K V T I D Y
20521 - ATGCTGAAATTTCATTCATGCTTTGGTGTAAGGATGGACATGTTGAAACCTTCTACCCAA - 20580
    - M L K F H S C F G V R M D M L K P S T Q
    - C * N F I H A L V * G W T C * N L L P K
       A E I S F M L W C K D G H V E T F Y P K
20581 - AACTACAAGCAAGTCAAGCGTGGCAACCAGGTGTTGCGATGCCTAACTTGTACAAGATGC - 20640
    -NYKQVKRGNQVLRCLTCTRC
      TTSKSSVATRCCDA*LVQDA
       L Q A S Q A W Q P G V A M P N L Y K M Q
20641 - AAAGAATGCTTCTTGAAAAGTGTGACCTTCAGAATTATGGTGAAAATGCTGTTATACCAA - 20700
    -KECFLKSVTFRIMVKMLLYQ
      K N A S * K V * P S E L W * K C C Y T K
       R M L L E K C D L Q N Y G E N A V I P K
20701 - AAGGAATAATGATGAATGTCGCAAAGTATACTCAACTGTGTCAATACTTAAATACACTTA - 20760
     -KE***MSQSILNCVNT*IHL
      R N N D E C R K V Y S T V S I L K Y T Y
       G I M M N V A K Y T Q L C Q Y L N T L T
20761 - CTTTAGCTGTACCCTACAACATGAGAGTTATTCACTTTGGTGCTGGCTCTGATAAAGGAG - 20820
     -L * L Y P T T * E L F T L V L A L I K E
      FSCTLQHESYSLWCWL**RS
       L A V P Y N M R V I H F G A G S D K G V
20821 - TTGCACCAGGTACAGCTGTGCTCAGACAATGGTTGCCAACTGGCACACTACTTGTCGATT - 20880
     - L H Q V Q L C S D N G C Q L A H Y L S I
      C T R Y S C A Q T M V A N W H T T C R F
       A P G T A V L R Q W L P T G T L L V D S
 20881 - CAGATCTTAATGACTTCGTCTCCGACGCAGATTCTACTTTAATTGGAGACTGTGCAACAG - 20940
     -QILMTSSPTQILL * LETVQQ
      RS * * LRLRRFYFNWRLCNS
       D L N D F V S D A D S T L I G D C A T V
 - Y I R L I N G T L L A I C M T L G P N
      T Y G * * M G P Y Y * R Y V * P * D Q T
       H T A N K W D L I I S D M Y D P R T K H
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21001 - ATGTGACAAAAGAGAATGACTCTAAAGAAGGGTTTTTCACTTATCTGTGTGGATTTATAA - 21060
    - M * Q K R M T L K K G F S L I C V D L *
    - C D K R E * L * R R V F H L S V W I Y K
- V T K E N D S K E G F F T Y L C G F I K
21061 - AGCAAAACTAGCCCTGGGTGGTTCTATAGCTGTAAAGATAACAGAGCATTCTTGGAATG - 21120
    -SKN * P W V V L * L * R * Q S I L G M
    - A K T S P G W F Y S C K D N R A F L E C
      Q K L A L G G S I A V K I T E H S W N A
21121 - CTGACCTTTACAAGCTTATGGGCCATTTCTCATGGTGGACAGCTTTTGTTACAAATGTAA - 21180
    -LTFTSLWAISHGGQLLLQM*
      * PLQAYGPFLMVDSFCYKCK
      D L Y K L M G H F S W W T A F V T N V N
21181 - ATGCATCATCGGAAGCATTTTTAATTGGGGCTAACTATCTTGGCAAGCCGAAGGAAC - 21240
    - M H H R K H F * L G L T I L A S R R N
     CIIIGSIFNWG*LSWQAEGT
       ASSSEAFLIGANYLGKPKEQ
21241 - AAATTGATGGCTATACCATGCTAACTACATTTTCTGGAGGAACACAAATCCTATCC - 21300
    - K L M A I P C M L T T F S G G T Q I L S
     N * W L Y H A C * L H F L E E H K S Y P
      I D G Y T M H A N Y I F W R N T N P I Q
21301 - AGTTGTCTTCCTATTCACTCTTTGACATGAGCAAATTTCCTCTTAAATTAAGAGGAACTG - 21360
    -SCLPIHSLT * ANFLLN * EEL
      V V F L F T L * H E Q I S S * I K R N C
    - LSSYSLFDMSKFPLKLRGTA
21361 - CTGTAATGTCTCTTAAGGAGAATCAAATCAATGATATGATTTATTCTCTTCTGGAAAAAG - 21420
    -L * C L L R R I K S M I * F I L F W K K
    - C N V S * G E S N Q * Y D L F S S G K R
      V M S L K E N Q I N D M I Y S L L E K G
21421 - GTAGGCTTATCATTAGAGAAAACAACAGAGTTGTGGTTTCAAGTGATATTCTTGTTAACA - 21480
    -VGLSLEKTTELWFQVIFLLT
      * A Y H * R K Q Q S C G F K * Y S C * Q
      RLIIRENNRVVVSSDILVNN
21481 - ACTAAACGAACATGTTTATTTTCTTATTATTTCTTACTCTCACTAGTGGTAGTGACCTTG - 21540
    -TKRTCLFSYYFLLSLVVTL
    - L N E H V Y F L I I S Y S H * W * * P *
      * T N M F I F L L F L T L T S G S D L D
21541 - ACCGGTGCACCACTTTTGATGATGTTCAAGCTCCTAATTACACTCAACATACTTCATCTA - 21600
    -TGAPLLMMFKLLITLNILHL
-PVHHF**CSSS*LHSTYFIY
       RCTTFDDVQAPNYTQHTSSM
-* G G F T I L M K F L D Q T L F I * L R
     - EGGLLS**NF*IRHSLFNSG
       R G V Y Y P D E I F R S D T L Y L T Q D
21661 - ATTTATTCTTCCATTTTATTCTAATGTTACAGGGTTTCATACTATTAATCATACGTTTG - 21720
     - I Y F F H F I L M L Q G F I L L I I R L
      FISSILF * CYRVSYY * SYVW
       L F L P F Y S N V T G F H T I N H T F G
21721 - GCAACCCTGTCATACCTTTTAAGGATGGTATTTATTTTGCTGCCACAGAGAAATCAAATG - 21780
     -ATLSYLLRMVFILLPQRNQM
      Q P C H T F * G W Y L F C C H R E I K C
       N P V I P F K D G I Y F A A T E K S N V
 21781 - TTGTCCGTGGTTGGGTTTTTGGTTCTACCATGAACAACAAGTCACAGTCGGTGATTATTA - 21840
     -LSVVGFLVLP*TTSHSR*LL
      C P W L G F W F Y H E Q Q V T V G D Y Y
       V R G W V F G S T M N N K S Q S V I I I
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21841 - TTAACAATTCTACTAATGTTGTTATACGAGCATGTAACTTTGAATTGTGTGACAACCCTT - 21900
    -LTILLMLLYEHVTLNCVTTL
    - * Q F Y * C C Y T S M * L * I V * Q P F - N N S T N V V I R A C N F E L C D N P F
21901 - TCTTTGCTGTTTCTAAACCCATGGGTACACAGACACATACTATGATATTCGATAATGCAT - 21960
    SLLFLNPWVHRHIL*YSIMH
    - L C C F * T H G Y T D T Y Y D I R * C I
       F A V S K P M G T Q T H T M I F D N A F
21961 - TTAATTGCACTTTCGAGTACATATCTGATGCCTTTTCGCTTGATGTTTCAGAAAAGTCAG - 22020
    -LIALSSTYLMPFRLMFQKSQ
      * L H F R V H I * C L F A * C F R K V R
       N C T F E Y I S D A F S L D V S E K S G
22021 - GTAATTTTAAACACTTACGAGAGTTTGTGTTTTAAAAATAAAGATGGGTTTCTCTATGTTT - 22080
    -VILNTYESLCLKIKMGFSMF
      * F * T L T R V C V * K * R W V S L C L
       N F K H L R E F V F K N K D G F L Y V Y
22081 - ATAAGGGCTATCAACCTATAGATGTAGTTCGTGATCTACCTTCTGGTTTTAACACTTTGA - 22140
    -IRAINL * M * F V I Y L L V L T L *
       * G L S T Y R C S S * S T F W F * H F E
       K G Y Q P I D V V R D L P S G F N T L K
22141 - AACCTATTTTTAAGTTGCCTCTTGGTATTAACATTACAAATTTTAGAGCCATTCTTACAG - 22200
    -NLFLSCLLVLTLQILEPFLQ
    - T Y F * V A S W Y * H Y K F * S H S Y S
      P I F K L P L G I N I T N F R A I L T A
22201 - CCTTTTCACCTGCTCAAGACATTTGGGGCACGTCAGCTGCAGCCTATTTTGTTGGCTATT - 22260
    - P F H L L K T F G A R Q L Q P I L L A I
    - L F T C S R H L G H V S C S L F C W L F
      F S P A Q D I W G T S A A A Y F V G Y L
22261 - TAAAGCCAACTACATTTATGCTCAAGTATGATGAAAATGGTACAATCACAGATGCTGTTG - 22320
    - * S Q L H L C S S M M K M V Q S Q M L L
    - K A N Y I Y A Q V * * K W Y N H R C C *
      K P T T F M L K Y D E N G T I T D A V D
22321 - ATTGTTCTCAAAATCCACTTGCTGAACTCAAATGCTCTGTTAAGAGCTTTGAGATTGACA - 22380
     -IVLKIHLLNSNALLRALRLT
      LFSKSTC*TQMLC*EL*D*Q
      C S Q N P L A E L K C S V K S F E I D K
22381 - AAGGAATTTACCAGACCTCTAATTTCAGGGTTGTTCCCTCAGGAGATGTTGTGAGATTCC - 22440
     -KEFTRPLISGLFPQEML*DS
     - R N L P D L * F Q G C S L R R C C E I P
      G I Y Q T S N F R V V P S G D V V R F P
22441 - CTAATATTACAAACTTGTGTCCTTTTGGAGAGGTTTTTAATGCTACTAAATTCCCTTCTG - 22500
     -LILQTCVLLERFLMLLNSLL
       * Y Y K L V S F W R G F * C Y * I P F C
      NITNLCPFGEVFNATKFPSV
22501 - TCTATGCATGGGAGAAAAAAAATTTCTAATTGTGTTGCTGATTACTCTGTGCTCTACA - 22560
     -SMHGREKKFLIVLLITLCST
       L C M G E K K N F * L C C * L L C A L Q
       Y A W E R K K I S N C V A D Y S V L Y N
22561 - ACTCAACATTTTTTCAACCTTTAAGTGCTATGGCGTTTCTGCCACTAAGTTGAATGATC - 22620
     -TQHFFQPLSAMAFLPLS*MI
      L N I F F N L * V L W R F C H * V E * S
       S T F F S T F K C Y G V S A T K L N D L
 22621 - TTTGCTTCTCCAATGTCTATGCAGATTCTTTTGTAGTCAAGGGAGATGATGTAAGACAAA - 22680
     -FASPMSMQILL*SREMM*DK
     - L L L Q C L C R F F C S Q G R * C K T N
        C F S N V Y A D S F V V K G D D V R Q I
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22681 - TAGCGCCAGGACAACTGGTGTTATTGCTGATTATAATTATAAATTGCCAGATGATTTCA - 22740
    - * R Q D K L V L L I I I I N C Q M I S
    - S A R T N W C Y C * L * L * I A R * F H
     A P G Q T G V I A D Y N Y K L P D D F M
22741 - TGGGTTGTCCTTGCTTGGAATACTAGGAACATTGATGCTACTTCAACTGGTAATTATA - 22800
    -W V V S L L G I L G T L M L L Q L V I I
    - G L C P C L E Y * E H * C Y F N W * L *
      G C V L A W N T R N I D A T S T G N Y N
-IINIGILD MASLGPLRETYL
     L * I * V S * T W Q A * A L * E R H I *
       Y K Y R Y L R H G K L R P F E R D I S N
22861 - ATGTGCCTTTCTCCCCTGATGGCAAACCTTGCACCCCACCTGCTCTTAATTGTTATTGGC - 22920
    -MCLSPLMANLAPHLLLIVIG
      C A F L P * W Q T L H P T C S * L L L A
      V P F S P D G K P C T P P A L N C Y W P
22921 - CATTAAATGATTATGGTTTTTACACCACTACTGGCATTGGCTACCAACCTTACAGAGTTG - 22980
    - H * M I M V F T P L L A L A T N L T E L
    - I K * L W F L H H Y W H W L P T L Q S C
    - LNDYGFYTTTGIGYQPYRVV
22981 - TAGTACTTTCTTTTGAACTTTTAAATGCACCGGCCACGGTTTGTGGACCAAAATTATCCA - 23040
    - * Y F L L N F * M H R P R F V D Q N Y P
    - S T F F * T F K C T G H G L W T K I I H
      V L S F E L L N A P A T V C G P K L S T
23041 - CTGACCTTATTAAGAACCAGTGTGTCAATTTTAATTTTAATGGACTCACTGGTACTGGTG - 23100
    -LTLLRTSVSILILMDSLVLV
      * P Y * E P V C Q F * F * W T H W Y W C
    - DLIKNQCVNFNGLTGTGV
23101 - TGTTAACTCCTTCTTCAAAGAGATTTCAACCATTTCAACAATTTGGCCGTGATGTTTCTG - 23160
    -C * L L Q R D F N H F N N L A V M F L
    - V N S F F K E I S T I S T I W P * C F *
      LTPSSKRFQPFQQFGRDVSD
23161 - ATTTCACTGATTCCGTTCGAGATCCTAAAACATCTGAAATATTAGACATTTCACCTTGCT - 23220
     -ISLIPFEILKHLKY*TFHLA
      F H * F R S R S * N I * N I R H F T L L
       FTDSVRDPKTSEILDISPCS
23221 - CTTTTGGGGGTGTAAGTGTAATTACACCTGGAACAAATGCTTCATCTGAAGTTGCTGTTC - 23280
     -LLGV*V*LHLEQMLHLKLLF
      F W G C K C N Y T W N K C F I * S C C S
       F G G V S V I T P G T N A S S E V A V L
23281 - TATATCAAGATGTTAACTGCACTGATGTTTCTACAGCAATTCATGCAGATCAACTCACAC - 23340
     -YIKMLTALMFLQQFMQINSH
       I S R C * L H * C F Y S N S C R S T H T
       Y Q D V N C T D V S T A I H A D Q L T P
 23341 - CAGCTTGGCGCATATATTCTACTGGAAACAATGTATTCCAGACTCAAGCAGGCTGTCTTA - 23400
     -QLGAYILLETMYSRLKQAVL
       S L A H I F Y W K Q C I P D S S R L S Y
       A W R I Y S T G N N V F Q T Q A G C L I
 23401 - TAGGAGCTGAGCATGTCGACACTTCTTATGAGTGCGACATTCCTATTGGAGCTGGCATTT - 23460
     -* E L S M S T L L M S A T F L L E L A F
       R S * A C R H F L * V R H S Y W S W H L
       G A E H V D T S Y E C D I P I G A G I C
 23461 - GTGCTAGTTACCATACAGTTTCTTTATTACGTAGTACTAGCCAAAAATCTATTGTGGCTT - 23520
     -V L V T I Q F L Y Y V V L A K N L L W L
      C * L P Y S F F I T * Y * P K I Y C G L
       A S Y H T V S L L R S T S Q K S I V A Y
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23521 - ATACTATGTCTTTAGGTGCTGATAGTTCAATTGCTTACTCTAATAACACCATTGCTATAC - 23580
    - I L C L * V L I V Q L L T L I T P L L Y
    - Y Y V F R C * * F N C L L * * H H C Y T
      T M S L G A D S S I A Y S N N T I A I P
23581 - CTACTAACTTTCAATTAGCATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAAACCT - 23640
    -LLTFQLALLQK*CLFLWLKP
    - Y * L F N * H Y Y R S N A C F Y G * N L
      T N F S I S I T T E V M P V S M A K T S
23641 - CCGTAGATTGTAATATGTACATCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCC - 23700
    - P * I V I C T S A E I L L N V L I C F S
     R R L * Y V H L R R F Y * M C * F A S P
      23701 - AATATGTAGCTTTTGCACACAACTAAATCGTGCACTCTCAGGTATTGCTGCTGAACAGG - 23760
    -N M V A F A H N * I V H S Q V L L L N R
     I W * L L H T T K S C T L R Y C C * T G
      Y G S F C T Q L N R A L S G I A A E Q D
23761 - ATCGCAACACGTGAAGTGTTCGCTCAAGTCAAACAAATGTACAAAACCCCAACTTTGA - 23820
    - I A T H V K C S L K S N K C T K P Q L *
      S Q H T * S V R S S Q T N V Q N P N F E
    - RNTREVFAQVKQMYKTPTLK
23821 - AATATTTTGGTGGTTTTAATTTTCACAAATATTACCTGACCCTCTAAAGCCAACTAAGA - 23880
    -NILVVLIFHKYYLTL*SQLR
    - I F W W F * F F T N I T * P S K A N * E
    - Y F G G F N F S Q I L P D P L K P T K R
23881 - GGTCTTTTATTGAGGACTTGCTCTTTAATAAGGTGACACTCGCTGATGCTTGGCTTCATGA - 23940
    -G L L R T C S L I R * H S L M L A S *
      V F Y * G L A L * * G D T R * C W L H E
       S F I E D L L F N K V T L A D A G F M K
23941 - AGCAATATGGCGAATGCCTAGGTGATATTAATGCTAGAGATCTCATTTGTGCGCAGAAGT - 24000
    -SNMANA * VILMLEIS FVRRS
     A I W R M P R * Y * C * R S H L C A E V
      Q Y G E C L G D I N A R D L I C A Q K F
24001 - TCAATGGACTTACAGTGTTGCCACCTCTGCTCACTGATGATATGATTGCTGCCTACACTG - 24060
    -SMDLQCCHLCSLMI*LLPTL
      Q W T Y S V A T S A H * * Y D C C L H C
       NGLTVLPPLLTDDMIAAYTA
24061 - CTGCTCTAGTTAGTGGTACTGCCACTGCTGGATGGACATTTGGTGCTGGCGCTGCTCTTC - 24120
    -LL*LVVLPLLDGHLVLALLF
-CSS*WYCHCWMDIWCWRCSS
       A L V S G T A T A G W T F G A G A A L Q
24121 - AAATACCTTTTGCTATGCAAATGGCATATAGGTTCAATGGCATTGGAGTTACCCAAAATG - 24180
    -KYLLLCKWHIGSMALELPKM
      N T F C Y A N G I * V Q W H W S Y P K C
       I P F A M Q M A Y R F N G I G V T Q N V
24181 - TTCTCTATGAGAACCAAAACAAATCGCCAACCAATTTAACAAGGCGATTAGTCAAATTC - 24240
    -FSMRTKNKSPTNLTRRLVKF
      S L * E P K T N R Q P I * Q G D * S N S
       L Y E N Q K Q I A N Q F N K A I S Q I Q
24241 - AAGAATCACTTACAACAACATCAACTGCATTGGGCAAGCTGCAAGACGTTGTTAACCAGA - 24300
     -KNHLQQHQLHWASCKTLLTR
      R I T Y N N I N C I G Q A A R R C * P E
       ESLTTTSTALGKLQDVVNQN
24301 - ATGCTCAAGCATTAAACACTTGTTAAACAACTTAGCTCTAATTTTGGTGCAATTTCAA - 24360
     -MLKH*THLLNNLALILVQFQ
      CSSIKHTC*TT*L*FWCNFK
       A Q A L N T L V K Q L S S N F G A I S S
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24361 - GTGTGCTAAATGATATCCTTTCGCGACTTGATAAAGTCGAGGCGGAGGTACAAATTGACA - 24420
    -V C * M I S F R D L I K S R R Y K L T
    - C A K * Y P F A T * * S R G G G T N * Q
      V L N D I L S R L D K V E A E V Q I D R
24421 - GGTTAATTACAGGCAGACTTCAAAGCCTTCAAACCTATGTAACACAACAACTAATCAGGG - 24480
    -G * L Q A D F K A F K P M * H N N * S G
    - V N Y R Q T S K P S N L C N T T N Q G
      L I T G R L Q S L Q T Y V T Q Q L I R A
24481 - CTGCTGAAATCAGGGCTTCTGCTAATCTTGCTGCTACTAAAATGTCTGAGTGTGTTCTTG - 24540
    -LLKSGLLLILLLKCLSVFL
     C * N Q G F C * S C C Y * N V * V C S W
       A E I R A S A N L A A T K M S E C V L G
24541 - GACAATCAAAAAGAGTTGACTTTTGTGGAAAGGGCTACCACCTTATGTCCTTCCCACAAG - 24600
    -DNQKELTFVERATTLCPSHK
    - TIKKS * LLWKGLPPYVLPTS
      Q S K R V D F C G K G Y H L M S F P Q A
24601 - CAGCCCCGCATGGTGTTCTTCCTACATGTCACGTATGTGCCATCCCAGGAGAGGAACT - 24660
    -QPRMVLSSYMSRMCHPRRGT
    - S P A W C C L P T C H V C A I P G E E L
       A P H G V V F L H V T Y V P S Q E R N F
24661 - TCACCACAGCGCCAGCAATTTGTCATGAAGGCAAAGCATACTTCCCTCGTGAAGGTGTTT - 24720
    -SPQRQQFVMKAKHTSLVKVF
    - H H S A S N L S * R Q S I L P S * R C F
       T T A P A I C H E G K A Y F P R E G V F
24721 - TTGTGTTTAATGGCACTTCTTGGTTTATTACACAGAGGAACTTCTTTTCTCCACAAATAA - 24780
    -LCLMALLGLLHRGTSFLHK*
      C V * W H F L V Y Y T E E L L F S T N N
       V F N G T S W F I T Q R N F F S P Q I I
24781 - TTACTACAGACAATACATTTGTCTCAGGAAATTGTGATGTCGTTATTGGCATCATTAACA - 24840
    -LLQTIHLSQEIVMSLLASLT
      YYRQYICLRKL*CRYWHH*Q
       T T D N T F V S G N C D V V I G I I N N
24841 - ACACAGTTTATGATCCTCTGCAACCTGAGCTTGACTCATTCAAAGAAGAGCTGGACAAGT - 24900
    -TQFMILCNLSLTHSKKSWTS
    - H S L * S S A T * A * L I Q R R A G Q V
      TVYDPLQPELDSFKEELDKY
24901 - ACTTCAAAAATCATCACCAGATGTTGATCTTGGCGACATTTCAGGCATTAACGCTT - 24960
    -TSKIIHHQMLILATFQALTL
    - L Q K S Y I T R C * S W R H F R H * R F
       F K N H T S P D V D L G D I S G I N A S
24961 - CTGTCGTCAACATTCAAAAAGAAATTGACCGCCTCAATGAGGTCGCTAAAAATTTAAATG - 25020
    -LSSTFKKKLTASMRSLKI*M
      CRQHSKRN*PPQ*GR*KFK*
       V V N I Q K E I D R L N E V A K N L N E
25021 - AATCACTCATTGACCTTCAAGAATTGGGAAAATATGAGCAATATATTAAATGGCCTTGGT - 25080
    -N H S L T F K N W E N M S N I L N G L G
    - I T H * P S R I G K I * A I Y * M A L V
       S L I D L Q E L G K Y E Q Y I K W P W Y
25081 - ATGTTTGGCTCGGCTTCATTGCTGGACTAATTGCCATCGTCATGGTTACAATCTTGCTTT - 25140
     -MFGSASLLD*LPSSWLQSCF
      C L A R L H C W T N C H R H G Y N L A L
       V W L G F I A G L I A I V M V T I L L C
25141 - GTTGCATGACTAGTTGTTGCAGTTGCCTCAAGGGTGCATGCTCTTGTGGTTCTTGCTGCA - 25200
     -VA*LVVAVASRVHALVVLAA
      L H D * L L Q L P Q G C M L L W F L L Q
       C M T S C C S C L K G A C S C G S C C K
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25201 - AGTTTGATGAGGATGACTCTGAGCCAGTTCTCAAGGGTGTCAAATTACATTACACATAAA - 25260
   -SLMRMTLSQFSRVSNYITHK
   - V * * G * L * A S S Q G C Q I T L H I N
   - FDEDDSEPVLKGVKLHYT * T
25261 - CGAACTTATGGATTTGTTTATGAGATTTTTTACTCTTGGATCAATTACTGCACAGCCAGT - 25320
   -RTYGFVYEIFYSWINYCTAS
   - E L M D L F M R F F T L G S I T A Q P V
      NLWICL*DFLLLDQLLHSQ*
25321 - AAAAATTGACAATGCTTCTCCTGCAAGTACTGTTCATGCTACAGCAACGATACCGCTACA - 25380
    - K N * Q C F S C K Y C S C Y S N D T A T
     K I D N A S P A S T V H A T A T I P L Q
      K L T M L L Q V L F M L Q Q R Y R Y K
25381 - AGCCTCACTCCCTTTCGGATGGCTTGTTATTGGCGTTGCATTTCTTGCTGTTTTTCAGAG - 25440
    -SLTPFRMACYWRCISCCFSE
     ASLPFGWLVIGVAFLAVFQS
     P H S L S D G L L L A L H F L L F F R A
25441 - CGCTACCAAAATAATTGCGCTCAATAAAAGATGGCAGCTAGCCCTTTATAAGGGCTTCCA - 25500
   -RYQNNCAQ*KMAASPL*GLP
    - A T K I I A L N K R W Q L A L Y K G F Q
    - LPK*LRSIKDGS*PFIRASS
25501 - GTTCATTTGCAATTTACTGCTGCTATTTGTTACCATCTATTCACATCTTTTGCTTGTCGC - 25560
    -V H L Q F T A A I C Y H L F T S F A C R
   - FICNLLLFVTIYSHLLLVA
    - SFAIYCCYLLPSIHIFCLSL
25561 - TGCAGGTAAGGAGGCGCAATTTTTGTACCTCTATGCCTTGATATATTTTCTACAATGCAT - 25620
    -CR*GGAIFVPLCLDIFSTMH
    - A G K E A Q F L Y L Y A L I Y F L Q C I
    - Q V R R R N F C T S M P * Y I F Y N A S
25621 - CAACGCATGTAGAATTATTATGAGATGTTGGCTTTGTTGGAAGTGCAAATCCAAGAACCC - 25680
    -QRM*NYYEMLALLEVQIQEP
    - N A C R I I M R C W L C W K C K S K N P
     THVELL * DVGFVGSANPRTH
-ITL*CQLLLAHT*L*LLY
    - L L Y D A N Y F V C W H T H N Y D Y C I
      Y F M M P T T L F A G T H I T M T T V Y
25741 - ACCATATAACAGTGTCACAGATACAATTGTCGTTACTGAAGGTGACGGCATTTCAACACC - 25800
    -TI*QCHRYNCRY*R*RHFNT
    - P Y N S V T D T I V V T E G D G I S T P
      H I T V S Q I Q L S L L K V T A F Q H Q
25801 - AAAACTCAAAGAAGACTACCAAATTGGTGGTTATTCTGAGGATAGGCACTCAGGTGTTAA - 25860
    -KTQRRLPNWWLF*G*ALRC*
     K L K E D Y Q I G G Y S E D R H S G V K
      N S K K T T K L V V I L R I G T Q V L K
25861 - AGACTATGTCGTTGTACATGGCTATTTCACCGAAGTTTACTACCAGCTTGAGTCTACACA - 25920
    -RLCRCTWLFHRSLLPA*VYT
     T M S L Y M A I S P K F T T S L S L H K
25921 - AATTACTACAGACACTGGTATTGAAAATGCTACATTCTTCATCTTTAACAAGCTTGTTAA - 25980
    -NYYRHWY*KCYILHL*QAC*
      I T T D T G I E N A T F F I F N K L V K
      L L Q T L V L K M L H S S S L T S L L K
25981 - AGACCCACCGAATGTGCAAATACACACAATCGACGGCTCTTCAGGAGTTGCTAATCCAGC - 26040
    -RPTECANTHNRRLFRSC * SS
     D P P N V Q I H T I D G S S G V A N P A
      THRMCKYTQSTALQELLIQQ
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26041 - AATGGATCCAATTTATGATGAGCCGACGACGACTACTAGCGTGCCTTTGTAAGCACAAGA - 26100
    -NGSNL * * ADDDY * R A F V S T R
    - M D P I Y D E P T T T T S V P L * A Q E
     WIQFMMSRRLLACLCKHKK
26101 - AAGTGAGTACGAACTTATGTACTCATTCGTTTCGGAAGAAACAGGTACGTTAATAGTTAA - 26160
    -K * V R T Y V L I R F G R N R Y V N S *
    - SEYELMYSFVSEETGTLIVN
     VSTNLCTHSFRKKQVR**LI
26161 - TAGCGTACTTCTTTTCTTGCTTTCGTGGTATTCTTGCTAGTCACACTAGCCATCCTTAC - 26220
    - * R T S F S C F R G I L A S H T S H P Y
     S V L L F L A F V V F L L V T L A I L T
      A Y F F F L L S W Y S C * S H * P S L L
26221 - TGCGCTTCGATTGTGTGCGTACTGCTGCAATATTGTTAACGTGAGTTTAGTAAAACCAAC - 26280
    -CASIVCVLLQYC*REFSKTN
    - A L R L C A Y C C N I V N V S L V K P T
     R F D C V R T A A I L L T * V * * N Q R
26281 - GGTTTACGTCTACTCGCGTGTTAAAAATCTGAACTCTTCTGAAGGAGTTCCTGATCTTCT - 26340
    -GLRLLAC * KSELF * RSS * SS
     V Y V Y S R V K N L N S S E G V P D L L
      FTSTRVLKI*TLLKEFLIFW
26341 - GGTCTAAACGAACTAACTATTATTATTATTCTGTTTGGAACTTTAACATTGCTTATCATG - 26400
    -GLNELTIIILFGTLTLLIM
     V * T N * L L L F C L E L * H C L S W
      S K R T N Y Y Y S V W N F N I A Y H G
26401 - GCAGACAACGGTACTATTACCGTTGAGGAGCTTAAACAACTCCTGGAACAATGGAACCTA - 26460
    - A D N G T I T V E E L K Q L L E Q W N L
      Q T T V L L P L R S L N N S W N N G T *
     R Q R Y Y Y R * G A * T T P G T M E P S
26461 - GTAATAGGTTTCCTATTCCTAGCCTGGATTATGTTACTACAATTTGCCTATTCTAATCGG - 26520
    -VIGFLFLAWIMLLQFAYSNR
-**VSYS*PGLCYYNLPILIG
      N R F P I P S L D Y V T T I C L F * S E
26521 - AACAGGTTTTTGTACATAATAAAGCTTGTTTTCCTCTGGCTCTTGTGGCCAGTAACACTT - 26580
    -NRFLYIIKLVFLWLLWPVTL
    - T G F C T * * S L F S S G S C G Q * H L
    - Q V F V H N K A C F P L A L V A S N T C
26581 - GCTTGTTTTGTGCTTGTCTACAGAATTAATTGGGTGACTGGCGGGATTGCGATT - 26640
    -ACFVLAVVYRINWVTGGIAI
    - L V L C L L S T E L I G * L A G L R L
      L F C A'C C C L Q N * L G D W R D C D C
-AMACIVGLMWLSYFVASFRL
     Q W L V L * A * C G L A T S L L P S G C
      NGLYCRLDVA*LLRCFLQAV
26701 - TTTGCTCGTACCCGCTCAATGTGGTCATTCAACCCAGAAACAACATTCTTCTCAATGTG - 26760
    -FARTRSMWSFNPETNILLNV
     L L V P A Q C G H S T Q K Q T F F S M C
      C S Y P L N V V I Q P R N K H S S Q C A
26761 - CCTCTCCGGGGGACAATTGTGACCAGACCGCTCATGGAAAGTGAACTTGTCATTGGTGCT - 26820
    -PLRGTIVTRPLMESELVIGA
     LSGGQL*PDRSWKVNLSLVL
      S P G D N C D Q T A H G K * T C H W C C
26821 - GTGATCATTCGTGGTCACTTGCGAATGGCCGGACACTCCCTAGGGCGCTGTGACATTAAG - 26880
    -VIIRGHLRMAGHSLGRCDIK
     * S F V V T C E W P D T P * G A V T L R
      D H S W S L A N G R T L P R A L * H * G
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FIG. 11 Con't

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26881 - GACCTGCCAAAAGAGATCACTGTGGCTACATCACGAACGCTTTCTTATTACAAATTAGGA - 26940
    -D L P K E I T V A T S R T L S Y Y K L G
    - T C Q K R S L W L H H E R F L I T N * E
     PAKRDHCGYITNAFLLQIRS
26941 - GCGTCGCAGCGTGTAGGCACTGATTCAGGTTTTGCTGCATACAACCGCTACCGTATTGGA - 27000
    - A S Q R V G T D S G F A A Y N R Y R I G
    - R R S V * A L I Q V L L H T T A T V L E
      V A A C R H * F R F C C I Q P L P Y W K
27001 - AACTATAAATTAAATACAGACCACGCCGGTAGCAACGACAATATTGCTTTGCTAGTACAG - 27060
    -NYKLNTDHAGSNDNIALLVQ
      TIN * I Q T T P V A T T I L L C * Y S
      L * I K Y R P R R * Q R Q Y C F A S T V
27061 - TAAGTGACAACAGATGTTTCATCTTGTTGACTTCCAGGTTACAATAGCAGAGATATTGAT - 27120
    - * V T T D V S S C * L P G Y N S R D I D
     K * Q Q M F H L V D F Q V T I A E I L I
      S D N R C F I L L T S R L Q * Q R Y * L
27121 - TATCATTATGAGGACTTTCAGGATTGCTATTTGGAATCTTGACGTTATAATAAGTTCAAT - 27180
    - Y H Y E D F Q D C Y L E S * R Y N K F N
     I I M R T F R I A I W N L D V I I S S I
      SL*GLSGLLFGILTL**VQ*
27181 - AGTGAGACAATTATTTAAGCCTCTAACTAAGAAGAATTATTCGGAGTTAGATGATGAAGA - 27240
    -SETII*ASN*EELFGVR**R
     V R Q L F K P L T K K N Y S E L D D E E
      * D N Y L S L * L R R I I R S * M M K N
27241 - ACCTATGGAGTTAGATTATCCATAAAACGAACATGAAAATTATTCTCTTCCTGACATTGA - 27300
    -TYGVRLSIKRT*KLFSS*H*
    - PMELDYP*NEHENYSLPDID
      LWS * IIHKTNMKIILFLTLI
27301 - TTGTATTTACATCTTGCGAGCTATATCACTATCAGGAGTGTGTTAGAGGTACGACTGTAC - 27360
    -LYLHLASYITIRSVLEVRLY
-CIYILRAISLSGVC*RYDCT
     V F T S C E L Y H Y Q E C V R G T T V L
27361 - TACTAAAAGAACCTTGCCCATCAGGAACATACGAGGGCAATTCACCATTTCACCCTCTTG - 27420
    - Y * K N L A H Q E H T R A I H H F T L L
    - T K R T L P I R N I R G Q F T I S P S C
      L K E P C P S G T Y E G N S P F H P L A
27421 - CTGACAATAAATTTGCACTAACTTGCACTAGCACACACTTTGCTTTTGCTTGTGCTGACG - 27480
    -LTINLH*LALAHTLLLLVLT
      * Q * I C T N L H * H T L C F C L C * R
      D N K F A L T C T S T H F A F A C A D G
27481 - GTACTCGACATACCTATCAGCTGCGTGCAAGATCAGTTTCACCAAAACTTTTCATCAGAC - 27540
    -VLDIPISCVQDQFHQNFSSD
-YSTYLSAACKISFTKTFHQT
       TRHTYQLRARSVSPKLFIRQ
27541 - AAGAGGAGGTTCAACAAGAGCTCTACTCGCCACTTTTTCTCATTGTTGCTGCTCTAGTAT - 27600
    -KRRFNKSSTRHFFSLLLL*Y
      R G G S T R A L L A T F S H C C C S S I
       E E V Q Q E L Y S P L F L I V A A L V F
-F * Y F A S P L R E R Q N E * A H F N *
      FNTLLHH*EKDRMNELTLID
      LILCFTIKRKTE * M S S L * L T
27661 - CTTCTATTTGTGCTTTTTAGCCTTTCTGCTATTCCTTGTTTTAATAATGCTTATTATATT - 27720
    -LLFVLFSLSAIPCFNNAYYI
    - FYLCFLAFLLFLVLIMLIIF
       SICAF * PFCYSLF * * CLLYF
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27721 - TTGGTTTTCACTCGAAATCCAGGATCTAGAAGAACCTTGTACCAAAGTCTAAACGAACAT - 27780
    -LVFTRNPGSRRTLYQSLNEH
-WFSLEIQDLEEPCTKV*TNM
      GFHSKSRI*KNLVPKSKRT*
27781 - GAAACTTCTCATTGTTTTGACTTGTATTTCTCTATGCAGTTGCATATGCACTGTAGTACA - 27840
    -ETSHCFDLYFSMQLHMHCST
    - K L L I V L T C I S L C S C I C T V V Q
       N F S L F * L V F L Y A V A Y A L * Y S
27841 - GCGCTGTGCATCTAATAAACCTCATGTGCTTGAAGATCCTTGTAAGGTACAACACTAGGG - 27900
    -ALCI**TSCA*RSL*GTTLG
     R C A S N K P H V L E D P C K V Q H * G
      A V H L I N L M C L K I L V R Y N T R G
27901 - GTAATACTTATAGCACTGCTTGGCTTTGTGCTCTAGGAAAGGTTTTACCTTTTCATAGAT - 27960
    -VILIALLGFVL*ERFYLFID
      * Y L * H C L A L C S R K G F T F S * M
       N T Y S T A W L C A L G K V L P F H R W
27961 - GGCACACTATGGTTCAAACATGCACACCTAATGTTACTATCAACTGTCAAGATCCAGCTG - 28020
    -GTLWFKHAHLMLLSTVKIQL
    - A H Y G S N M H T * C Y Y Q L S R S S W
      H T M V Q T C T P N V T I N C Q D P A G
28021 - GTGGTGCGCTTATAGCTAGGTGTTGGTACCTTCATGAAGGTCACCAAACTGCTGCATTTA - 28080
    -VVRL*LGVGTFMKVTKLLHL
      W C A Y S * V L V P S * R S P N C C I *
      G A L I A R C W Y L H E G H Q T A A F R
28081 - GAGACGTACTTGTTTTTAAATAAACGAACAAATTAAAATGTCTGATAATGGACCCCAA - 28140
    -ETYLLF*INEQIKMSDNGPQ
    - R R T C C F K * T N K L K C L I M D P N
      D V L V V L N K R T N * N V * * W T P I
28141 - TCAAACCAACGTAGTGCCCCCCGCATTACATTTGGTGGACCCACAGATTCAACTGACAAT - 28200
    -SNQRSAPRITFGGPTDSTDN
      \begin{smallmatrix}&&&-\\Q&&T&&N&&V&&P&&P&&A&&L&&H&&L&&V&&D&&P&&Q&&I&&Q&&L&&T&&I&\\\end{smallmatrix}
       K P T * C P P H Y I W W T H R F N * Q *
28201 - AACCAGAATGGAGGACGCAATGGGGCCAAGGCCAAAACAGCGCCCAAGGTTTACCC - 28260
    -NQNGGRNGARPKQRRPQGLP
    - T R M E D A M G Q G Q N S A D P K V Y P
      PEWRTQWGKAKTAPTPRFTQ
28261 - AATAATACTGCGTCTTGGTTCACAGCTCTCACTCAGCATGGCAAGGAGGAACTTAGATTC - 28320
    -NNTASWFTALTQHGKEELRF
      I I L R L G S Q L S L S M A R R N L D S
       * Y C V L V H S S H S A W Q G G T * I P
28321 - CCTCGAGGCCAGGGCGTTCCAATCAACACCAATAGTGGTCCAGATGACCAAATTGGCTAC - 28380
     - P R G Q G V P I N T N S G P D D Q I G Y
      L E A R A F Q S T P I V V Q M T K L A T
S R P G R S N Q H Q * W S R * P N W L L
28381 - TACCGAAGAGCTACCCGACGAGTTCGTGGTGGTGACGGCAAAATGAAAGAGCTCAGCCCC - 28440
     - Y R R A T R R V R G G D G K M K E L S P
       TEELPDEFVVVTAK*KSSAP
       PKSYPTSSWW*RQNERAQPQ
28441 - AGATGGTACTTCTATTACCTAGGAACTGGCCCAGAAGCTTCACTTCCCTACGGCGCTAAC - 28500
     -R W Y F Y Y L G T G P E A S L P Y G A N
      D G T S I T * E L A Q K L H F P T A L T
       MVLLLPRNWPRSFTSLRR*Q
28501 - AAAGAAGGCATCGTATGGGTTGCAACTGAGGGAGCCTTGAATACACCCAAAGACCACATT - 28560
     -KEGIVWVATEGALNTPKDHI
      KKASYGLQLREP*IHPKTTL
       RRHRMGCN*GSLEYTQRPHW
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28561 - GGCACCCGCAATCCTAATAACAATGCTGCCACCGTGCTACAACTTCCTCAAGGAACAACA - 28620
    -GTRNPNNNAATVLQLPQGTT
    - A P A I L I T M L P P C Y N F L K E Q H
     HPQS**QCCHRATTSSRNNI
28621 - TTGCCAAAAGGCTTCTACGCAGAGGGAAGCAGAGGCGGCAGTCAAGCCTCTTCTCGCTCC - 28680
    - L P K G F Y A E G S R G G S Q A S S R S
    - C Q K A S T Q R E A E A A V K P L L A P
      A K R L L R R G K Q R R Q S S L F S L L
28681 - TCATCACGTAGTCGCGGTAATTCAAGAAATTCAACTCCTGGCAGCAGTAGGGGAAATTCT - 28740
    -SSRSRGNSRNSTPGSSRGNS
    - H H V V A V I Q E I Q L L A A V G E I L
      I T * S R * F K K F N S W Q Q * G K F S
28741 - CCTGCTCGAATGGCTAGCGGAGGTGGTGAAACTGCCCTCGCGCTATTGCTGCTAGACAGA - 28800
    - P A R M A S G G G E T A L A L L L D R
     L L E W L A E V V K L P S R Y C C * T D
      C S N G * R R W * N C P R A I A A R Q I
28801 - TTGAACCAGCTTGAGAGCAAAGTTTCTGGTAAAGGCCAACAACAACAAGGCCAAACTGTC - 28860
    -LNQLESKVSGKGQQQQGQTV
     * T S L R A K F L V K A N N N K A K L S
      E P A * E Q S F W * R P T T T R P N C H
28861 - ACTAAGAAATCTGCTGCTGAGGCATCTAAAAAGCCTCGCCAAAAACGTACTGCCACAAAA - 28920
    -TKKSAAEASKKPRQKRTATK
    - L R N L L R H L K S L A K N V L P Q N
      * E I C C * G I * K A S P K T Y C H K T
28921 - CAGTACAACGTCACTCAAGCATTTGGGAGACGTGGTCCAGAACAAACCCAAGGAAATTTC - 28980
    -QYNVTQAFGRRGPEQTQGNF
     S T T S L K H L G D V V Q N K P K E I S
      V Q R H S S I W E T W S R T N P R K F R
28981 - GGGGACCAAGACCTAATCAGACAAGGAACTGATTACAAACATTGGCCGCAAATTGCACAA - 29040
    -G D Q D L I R Q G T D Y K H W P Q I A Q
     G T K T * S D K E L I T N I G R K L H N
       G P R P N Q T R N * L Q T L A A N C T I
29041 - TTTGCTCCAAGTGCCTCTGCATTCTTTGGAATGTCACGCATTGGCATGGAAGTCACACCT - 29100
    -FAPSASAFFGMSRIGMEVTP
      L L Q V P L H S L E C H A L A W K S H L
       C S K C L C I L W N V T H W H G S H T F
29101 - TCGGGAACATGGCTGACTTATCATGGAGCCATTAAATTGGATGACAAAGATCCACAATTC - 29160
    -SGTWLTYHGAIKLDDKDPQF
    - REHG * LIMEPLNWMTKIHNS
       G N M A D L S W S H * I G * Q R S T I Q
29161 - AAAGACAACGTCATACTGCTGAACAAGCACATTGACGCATACAAAACATTCCCACCAACA - 29220
    -KDNVILLNKHIDAYKTFPPT
    - K T T S Y C * T S T L T H T K H S H Q Q
       R Q R H T A E Q A H * R I Q N I P T N R
29221 - GAGCCTAAAAAGGACAAAAGAAAAGACTGATGAAGCTCAGCCTTTGCCGCAGAGACAA - 29280
    -EPKKDKKKTDEAQPLPQRQ
      SLKRTKRKRLMKLSLCRRDK
       A * K G Q K E K D * * S S A F A A E T K
29281 - AAGAAGCAGCCCACTGTGACTCTTCTTCCTGCGGCTGACATGGATGATTTCTCCAGACAA - 29340
    -KKQPTVTLLPAADMDDFSRQ
      RSSPL*LFFLRLTWMISPDN
      E A A H C D S S S C G * H G * F L Q T T
29341 - CTTCAAAATTCCATGAGTGGAGCTTCTGCTGATTCAACTCAGGCATAAACACTCATGATG - 29400
    -LQNSMSGASADSTQA*TLMM
    - F K I P * V E L L I Q L R H K H S * *
       SKFHEWSFC*FNSGINTHDD
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29401 - ACCACACAAGGCAGATGGGCTATGTAAACGTTTTCGCAATTCCGTTTACGATACATAGTC - 29460
   - P H K A D G L C K R F R N S V Y D T * S
   - HTRQMGYVNVFAIPFTIHSL
29461 - TACTCTTGTGCAGAATGAATTCTCGTAACTAAACAGCACAAGTAGGTTTAGTTAACTTTA - 29520
   -YSCAE*ILVTKQHK*V*LTL
   - TLVQNEFS * LNSTSRFS * L *
   - L L C R M N S R N * T A Q V G L V N F N
29521 - ATCTCACATAGCAATCTTTAATCAATGTGTAACATTAGGGAGGACTTGAAAGAGCCACCA - 29580
   -ISHSNL*SMCNIREDLKEPP
   - S H I A I F N Q C V T L G R T * K S H H
    - LT * Q S L I N V * H * G G L E R A T T
29581 - CATTTTCATCGAGGCCACGCGGAGTACGATCGAGGGTACAGTGAATAATGCTAGGGAGAG - 29640
    - H F H R G H A E Y D R G Y S E * C * G E
    - I F I E A T R S T I E G T V N N A R E S
   - FSSRPRGVRSRVQ*IMLGRA
29641 - CTGCCTATATGGAAGAGCCCTAATGTGTAAAATTAATTTTAGTAGTGCTATCCCCATGTG - 29700
    -LPIWKSPNV * N * F * * C Y P H V
    - CLYGRALMCKINFSSAIPM *
    - AYMEEP * CVKLILVVLSPCD
- 29742
    - I L I A S * E N D K K K K X
    - F * * L L R R M T K K K X
     FNSFLGE * QKKKKX
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FIG. 11 Con't

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1 - TTTTTTTTTTTTTTTTTCCTAAGAAGCTATTAAAATCACATGGGGATAGCACTA - 60
  -FFFFFVILLRSY*NHMGIAL
    FFFFLSFS*EAIKITWG*HY
    F F F C H S P K K L L K S H G D S T T
61 - CTAAAATTAATTTTACACATTAGGGCTCTTCCATATAGGCAGCTCTCCCTAGCATTATTC - 120
  -LKLILHIRALPYRQLSLALF
   * N * F Y T L G L F H I G S S P * H Y S
    KINFTH * G S S I * A A L P S I I H
121 - ACTGTACCCTCGATCGTACTCCGCGTGGCCTCGATGAAAATGTGGTGGCTCTTTCAAGTC - 180
  -TVPSIVLRVASMKMWWLFQV
   L Y P R S Y S A W P R * K C G G S F K S
    C T L D R T P R G L D E N V V A L S S P
181 - CTCCCTAATGTTACACATTGATTAAAGATTGCTATGTGAGATTAAAGTTAACTAAACCTA - 240
  -LPNVTH*LKIAM*D*S*LNL
    SLMLHID * RLLCEIK V N * T Y
    P * C Y T L I K D C Y V R L K L T K P T
241 - CTTGTGCTGTTTAGTTACGAGAATTCATTCTGCACAAGAGTAGACTATGTATCGTAAACG - 300
  -LVLFSYENSFCTRVDYVS*T
    L C C L V T R I H S A Q E * T M Y R K R
    CAV*LREFILHKSRLCIVNG
-ELRKRLHSPSALCGHHECLC
   NCENVYIAHLPCVVIMSVYA
     IAKTFT * PICLVWSS * V F M P
361 - CTGAGTTGAATCAGCAGAAGCTCCACTCATGGAATTTTGAAGTTGTCTGGAGAAATCATC - 420
  -LS * ISRSSTHGILK LSGEII
     V E S A E A P L M E F * S C L E K S S
     ELNQQKLHSWNFEVVWRNHP
421 - CATGTCAGCCGCAGGAAGAAGAGTCACAGTGGGCTGCTTCTTTTGTCTCTGCGGCAAAGG - 480
  -HVSRRKKSHSGLLLLSLRQR
    M S A A G R R V T V G C F F C L C G K G
  - CQPQEEESQWAASFVSAAKA
481 - CTGAGCTTCATCAGTCTTTTTCTTTTTGTCCTTTTTAGGCTCTGTTGGTGGGAATGTTTT - 540
  -LSFISLFLFVLFRLCWWECF
    * A S S V F F F L S F L G S V G G N V L
     ELHQSFSFCPF*ALLVGMFC
541 - GTATGCGTCAATGTGCTTGTTCAGCAGTATGACGTTGTCTTTGAATTGTGGATCTTTGTC - 600
  -VCVNVLVQQYDVVFELWIFV
    Y A S M C L F S S M T L S L N C G S L S
     MRQCACSAV*RCL*IVDLCH
601 - ATCCAATTTAATGGCTCCATGATAAGTCAGCCATGTTCCCGAAGGTGTGACTTCCATGCC - 660
  -I Q F N G S M I S Q P C S R R C D F H A
    S N L M A P * * V S H V P E G V T S M P
     PI * W L H D K S A M F P K V * L P C Q
661 - AATGCGTGACATTCCAAAGAATGCAGAGGCACTTGGAGCAAATTGTGCAATTTGCGGCCA - 720
  -NA*HSKECRGTWSKLCNLRP
    M R D I P K N A E A L G A N C A I C G Q
     CVTFQRMQRHLEQIVQFAAN
721 - ATGTTTGTAATCAGTTCCTTGTCTGATTAGGTCTTGGTCCCCGAAATTTCCTTGGGTTTG - 780
  -MFVISSLSD*VLVPEISLGL
    C L * S V P C L I R S W S P K F P W V C
     V C N Q F L V * L G L G P R N F L G F V
781 - TTCTGGACCACGTCTCCCAAATGCTTGAGTGACGTTGTACTGTTTTGTGGCAGTACGTTT - 840
  -FWTTSPKCLSDVVLFCGSTF
  - S G P R L P N A * V T L Y C F V A V R F
     L D H V S Q M L E * R C T V L W Q Y V F
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841 - TTGGCGAGGCTTTTTAGATGCCTCAGCAGCAGATTTCTTAGTGACAGTTTGGCCTTGTTG - 900
   -LARLFRCLSSRFLSDSLALL
   - W R G F L D A S A A D F L V T V W P C C
      GEAF * M P Q Q I S * * Q F G L V V
901 - TTGTTGGCCTTTACCAGAAACTTTGCTCTCAAGCTGGTTCAATCTGTCTAGCAGCAATAG - 960
   -LLAFTRNFALKLVQSV*QQ*
   - C W P L P E T L L S S W F N L S S S N S
      V G L Y Q K L C S Q A G S I C L A A I A
961 - CGCGAGGGCAGTTTCACCACCTCCGCTAGCCATTCGAGCAGGAGAATTTCCCCTACTGCT - 1020
   -REGSFTTSASHSSRRISPTA
    A R A V S P P L A I R A G E F P L L L
      RGQFHHLR*PFEQENFPYCC
1021 - GCCAGGAGTTGAATTTCTTGAATTACCGCGACTACGTGATGAGGAGCGAGAAGAGGCTTG - 1080
   -ARS * IS * ITATT * * GARRGL
    PGVEFLELPRLRDEEREEA*
      Q E L N F L N Y R D Y V M R S E K R L D
1081 - ACTGCCGCCTCTGCTTCCCTCTGCGTAGAAGCCTTTTGGCAATGTTGTTCCTTGAGGAAG - 1140
   -TAASASLCVEAFWQCCSLRK
     L P P L L P S A * K P F G N V V P * G S
     C R L C F P L R R S L L A M L F L E E V
1141 - TTGTAGCACGGTGGCAGCATTGTTATTAGGATTGCGGGTGCCAATGTGGTCTTTGGGTGT - 1200
   -L * H G G S I V I R I A G A N V V F G C
     C S T V A A L L L G L R V P M W S L G V
     V A R W Q H C Y * D C G C Q C G L W V Y
1201 - ATTCAAGGCTCCCTCAGTTGCAACCCATACGATGCCTTCTTTGTTAGCGCCGTAGGGAAG - 1260
   -I Q G S L S C N P Y D A F F V S A V G K
     F K A P S V A T H T M P S L L A P * G S
      S R L P Q L Q P I R C L L C * R R E V
1261 - TGAAGCTTCTGGGCCAGTTCCTAGGTAATAGAAGTACCATCTGGGGCTGAGCTCTTTCAT - 1320
   - * S F W A S S * V I E V P S G A E L F H
   - E A S G P V P R * * K Y H L G L S S F I
     K L L G Q F L G N R S T I W G * A L S F
1321 - TTTGCCGTCACCACGAACTCGTCGGGTAGCTCTTCGGTAGTAGCCAATTTGGTCATC - 1380
   -FAVTTTNSSGSSSVVANLVI
   - L P S P P R T R R V A L R * * P I W S S
     CRHHHELVG*LFGSSQFGHL
1381 - TGGACCACTATTGGTGTTGATTGGAACGCCCTGGCCTCGAGGGAATCTAAGTTCCTCCTT - 1440
   -W T T I G V D W N A L A S R E S K F L L
     G P L L V L I G T P W P R G N L S S S L
      D H Y W C * L E R P G L E G I * V P P C
1441 - GCCATGCTGAGTGAGAGCTGTGAACCAAGACGCAGTATTATTGGGTAAACCTTGGGGTCG - 1500
    -AMLSESCEPRRSIIG*TLGS
     PC * V R A V N Q D A V L L G K P W G R
      HAE*EL*TKTQYYWVNLGVG
1501 - GCGCTGTTTTGGCCTTGCCCCATTGCGTCCTCCATTCTGGTTATTGTCAGTTGAATCTGT - 1560
   -ALFWPCPIASSILVIVS * I C
     R C F G L A P L R P P F W L L S V E S V
      A V L A L P H C V L H S G Y C Q L N L W
1561 - GGGTCCACCAAATGTAATGCGGGGGGCACTACGTTGGTTTGATTGGGGTCCATTATCAGA - 1620
    -GSTKCNAGGTTLV * LGSIIR
     G P P N V M R G A L R W F D W G P L S D
      V H Q M * C G G H Y V G L I G V H Y Q T
1621 - CATTTTAATTTGTTCGTTTATTTAAAACAACAAGTACGTCTCTAAATGCAGCAGTTTGGT - 1680
    - H F N L F V Y L K Q Q V R L * M Q Q F G
     I L I C S F I * N N K Y V S K C S S L V
        * F V R L F K T T S T S L N A A V W *
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1681 - GACCTTCATGAAGGTACCAACACCTAGCTATAAGCGCACCACCAGCTGGATCTTGACAGT - 1740
   -DLHEGTNT * L * A H H Q L D L D S
   - T F M K V P T P S Y K R T T S W I L T V
    PS * R Y Q H L A I S A P P A G S * Q L
1741 - TGATAGTAACATTAGGTGTGCATGTTTGAACCATAGTGTGCCATCTATGAAAAGGTAAAA - 1800
   - * * * H * V C M F E P * C A I Y E K V K
   - D S N I R C A C L N H S V P S M K R *
     I V T L G V H V * T I V C H L * K G K T
1801 - CCTTTCCTAGAGCACAAAGCCAAGCAGTGCTATAAGTATTACCCCTAGTGTTGTACCTTA - 1860
   - P F L E H K A K Q C Y K Y Y P * C C T L
    L S * S T K P S S A I S I T P S V V P Y
      FPRAQSQAVL*VLPLVLYLT
1861 - CAAGGATCTTCAAGCACATGAGGTTTATTAGATGCACAGCGCTGTACTACAGTGCATATG - 1920
   -QGSSST*GLLDAQRCTTVHM
     K D L Q A H E V Y * M H S A V L Q C I C
     RIFKHMRFIRCTALYYSAYA
1921 - CAACTGCATAGAGAAATACAAGTCAAAACAATGAGAAGTTTCATGTTCGTTTAGACTTTG - 1980
   -QLHREIQVKTMRSFMFV*TL
     NCIEKYKSKQ*EVSCSFRLW
     T A * R N T S Q N N E K F H V R L D F G
1981 - GTACAAGGTTCTTCTAGATCCTGGATTTCGAGTGAAAACCAAAATATAATAAGCATTATT - 2040
   -V Q G S S R S W I S S E N Q N I I S I I
     Y K V L L D P G F R V K T K I * * A L L
      T R F F * I L D F E * K P K Y N K H Y *
2041 - AAAACAAGGAATAGCAGAAAGGCTAAAAAGCACAAATAGAAGTCAATTAAAGTGAGCTCA - 2100
   - K T R N S R K A K K H K * K S I K V S S
   - K Q G I A E R L K S T N R S Q L K * A H
     NKE * QKG * KAQIEVN * SELI
2101 - TTCATTCTGTCTTTCTCTTAATGGTGAAGCAAAGTATTAAAAATACTAGAGCAGCAACAA - 2160
   -FILSFS * W * S K V L K I L E Q Q Q
     S F C L S L N G E A K Y * K Y * S S N N
     H S V F L L M V K Q S I K N T R A A T M
2161 - TGAGAAAAAGTGGCGAGTAGAGCTCTTGTTGAACCTCCTCTTGTCTGATGAAAAGTTTTG - 2220
   - * E K V A S R A L V E P P L V * * K V L
   - E K K W R V E L L N L L L S D E K F W
      R K S G E * S S C * T S S C L M K S F G
2221 - GTGAAACTGATCTTGCACGCAGCTGATAGGTATGTCGAGTACCGTCAGCACAAGCAAAAG - 2280
   -V K L I L H A A D R Y V E Y R Q H K Q K
     * N * S C T Q L I G M S S T V S T S K S
      E T D L A R S * * V C R V P S A Q A K A
2281 - CAAAGTGTGCTAGTGCAAGTTAGTGCAAATTTATTGTCAGCAAGAGGGTGAAATGGTG - 2340
    -QSVC*CKLVQIYCQQEGEMV
    KVCASAS * CKFIVSKRVKW *
     KCVLVQVSANLLSARG*NGE
2341 - AATTGCCCTCGTATGTTCCTGATGGGCAAGGTTCTTTTAGTAGTACAGTCGTACCTCTAA - 2400
    -NCPRMFLMGKVLLVVQSYL*
     I A L V C S * W A R F F * * Y S R T S N
      L P S Y V P D G Q G S F S S T V V P L T
- H T P D S D I A R K M * I Q S M S G R E
     T L L I V I * L A R C K Y N Q C Q E E N
      H S * * * Y S S Q D V N T I N V R K R I
2461 - TAATTTCATGTTCGTTTTATGGATAATCTAACTCCATAGGTTCTTCATCATCTAACTCC - 2520
    - * F S C S F Y G * S N S I G S S S N S
     N F H V R F M D N L T P * V L H H L T P
      IFMFVLWII*LHRFFII*LR
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2521 - GAATAATTCTTCTTAGTTAGAGGCTTAAATAATTGTCTCACTATTGAACTTATTATAACG - 2580
   -E * F F L V R G L N N C L T I E L I I T
   - N N S S * L E A * I I V S L L N L L * R
    IILLS * R L K * L S H Y * T Y Y N V
2581 - TCAAGATTCCAAATAGCAATCCTGAAAGTCCTCATAATGATAATCAATATCTCTGCTATT - 2640
   -SRFQIAILKVLIMIINISAI
   - Q D S K * Q S * K S S * * * S I S L L L
     KIPNSNPESPHNDNQYLCYC
2641 - GTAACCTGGAAGTCAACAAGATGAAACATCTGTTGTCACTTACTGTACTAGCAAAGCAAT - 2700
   -VTWKSTR*NICCHLLY*QSN
     * P G S Q Q D E T S V V T Y C T S K A I
     N L E V N K M K H L L S L T V L A K Q Y
2701 - ATTGTCGTTGCTACCGGCGTGGTCTGTATTTAATTTATAGTTTCCAATACGGTAGCGGTT - 2760
   -IVVATGVVCI*FIVSNTVAV
    LSLLPAWSVFNL*FPIR*RL
     CRCYRRGLYLIYSFQYGSGC
2761 - GTATGCAGCAAAACCTGAATCAGTGCCTACACGCTGCGACGCTCCTAATTTGTAATAAGA - 2820
   -V C S K T * I S A Y T L R R S * F V I R
     Y A A K P E S V P T R C D A P N L * * E
      MOONLNQCLHAATLLICNKK
2821 - AAGCGTTCGTGATGTAGCCACAGTGATCTCTTTTGGCAGGTCCTTAATGTCACAGCGCCC - 2880
   -KRS * CSHSDLF W Q V L N V T A P
     S V R D V A T V I S F G R S L M S Q R P
   - AFVM*PQ*SLLAGP*CHSAL
2881 - TAGGGAGTGTCCGGCCATTCGCAAGTGACCACGAATGATCACAGCACCAATGACAAGTTC - 2940
   - * G V S G H S Q V T T N D H S T N D K F
   - R E C P A I R K * P R M I T A P M T S S
   - GSVRPFASDHE * SQHQ * QVH
2941 - ACTTTCCATGAGCGGTCTGGTCACAATTGTCCCCCGGAGAGGCACATTGAGAAGAATGTT - 3000
   -TFHERSGHNCPPERHIEKNV
   - L S M S G L V T I V P R R G T L R R M F
   - FP * A V W S Q L S P G E A H * E E C L
-CFWVE*PH*AGTSKQPEGSN
   - V S G L N D H I E R V R A N S L K E A T
      F L G * M T T L S G Y E Q T A * R K Q R
3061 - GAAGTAGCTAAGCCACATCAAGCCTACAATACAAGCCATTGCAATCGCAATCCCGCCAGT - 3120
   -EVAKPHQAYNTSHCNRNPAS
   - K * L S H I K P T I Q A I A I A I P P V
      SS*ATSSLQYKPLQSQSRQS
- H P I N S V D N S K H K T S K C Y W P Q
      \begin{smallmatrix} T & Q & L & I & L & * & T & T & A & S & T & K & Q & A & S & V & T & G & H & K \\ \end{smallmatrix} 
      P N * F C R Q Q A Q N K Q V L L A T R
3181 - GAGCCAGAGGAAAACAAGCTTTATTATGTACAAAAACCTGTTCCGATTAGAATAGGCAAA - 3240
   -EPEENKLYYVQKPVPIRIGK
     S Q R K T S F I M Y K N L F R L E * A N
      ARGKQALLCTKTCSD*NRQI
3241 - TTGTAGTAACATAATCCAGGCTAGGAATAGGAAACCTATTACTAGGTTCCATTGTTCCAG - 3300
   - L * * H N P G * E * E T Y Y * V P L F Q
     C S N I I Q A R N R K P I T R F H C S R
     V V T * S R L G I G N L L L G S I V P G
3301 - GAGTTGTTTAAGCTCCTCAACGGTAATAGTACCGTTGTCTGCCATGATAAGCAATGTTAA - 3360
   -ELFKLLNGNSTVVCHDKQC *
   - S C L S S S T V I V P L S A M I S N V K
      V V * A P Q R * * Y R C L P * * A M L K
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FIG. 12 Con't

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3361 - AGTTCCAAACAGAATAATAATAATAGTTAGTTCGTTTAGACCAGAAGATCAGGAACTCCT - 3420
   -SSKQNNNNS*FV*TRRSGTP
   - V P N R I I I I V S S F R P E D Q E L L
    FQTE****LVRLDQKIRNSF
3421 - TCAGAAGAGTTCAGATTTTTAACACGCGAGTAGACGTAAACCGTTGGTTTTACTAAACTC - 3480
   -SEEFRFLTRE*TVGFTKL
   - Q K S S D F * H A S R R K P L V L L N S
    RRVQIFNTRVDVNRWFY*TH
3481 - ACGTTAACAATATTGCAGCAGTACGCACACAATCGAAGCGCAGTAAGGATGGCTAGTGTG - 3540
   -TLTILQQYAHNRSAVRMASV
    R * Q Y C S S T H T I E A Q * G W L V *
    V N N I A A V R T Q S K R S K D G * C D
3541 - ACTAGCAAGAATACCACGAAAGCAAGAAAAAGAAGTACGCTATTAACTATTAACGTACCT - 3600
   -TSKNTTKARKRSTLLTINVP
    LARIPRKQEKEVRY*LLTYL
    * Q E Y H E S K K K Y A I N Y * R T C
3601 - GTTTCTTCCGAAACGAATGAGTACATAAGTTCGTACTCACTTTCTTGTGCTTACAAAGGC - 3660
   -VSSETNEYISSYSLSCAYKG
    FLPKRMST*VRTHFLVLTKA
     FFRNE*VHKFVLTFLCLQRH
3661 - ACGCTAGTAGTCGTCGTCGGCTCATCATAAATTGGATCCATTGCTGGATTAGCAACTCCT - 3720
   -TLVVVVGSS*IGSIAGLATP
    R * * S S S A H H K L D P L L D * Q L L
     ASSRRRLIINWIHCWISNS *
3721 - GAAGAGCCGTCGATTGTGTATTTGCACATTCGGTGGGTCTTTAACAAGCTTGTTAAAG - 3780
   -EEPSIVCICTFGGSLTSLLK
   - K S R R L C V F A H S V G L * Q A C * R
   - RAVDCVYLHIRWVFNKLVKD
3781 - ATGAAGAATGTAGCATTTTCAATACCAGTGTCTGTAGTAATTTGTGTAGACTCAAGCTGG - 3840
   - M K N V A F S I P V S V V I C V D S S W
     * R M * H F Q Y Q C L * * F V * T Q A G
   - EECSIFNTSVCSNLCRLKLV
3841 - TAGTAAACTTCGGTGAAATAGCCATGTACAACGACATAGTCTTTAACACCTGAGTGCCTA - 3900
   - * * T S V K * P C T T T * S L T P E C L
   - S K L R * N S H V Q R H S L * H L S A Y
    V N F G E I A M Y N D I V F N T * V P I
3901 - TCCTCAGAATAACCACCAATTTGGTAGTCTTCTTTGAGTTTTGGTGTTGAAATGCCGTCA - 3960
   -SSE*PPIW*SSLSFGVEMPS
    PQNNHQFGSLL*VLKCRH
     LRITTNLVVFFEFWC*NAVT
3961 - CCTTCAGTAACGACAATTGTATCTGTGACACTGTTATATGGTATACAGTAGTCATAGTTA - 4020
   -PSVTTIVSVTLLYGIQ*S*L
    L Q * R Q L Y L * H C Y M V Y S S H S Y
      F S N D N C I C D T V I W Y T V V I V M
4021 - TGTGTGTGCCAGCAAACAAGTAGTTGGCATCATAAAGTAATGGGTTCTTGGATTTGCAC - 4080
   -CVCQQTK*LAS*SNGFLDLH
     V C A S K Q S S W H H K V M G S W I C T
     C V P A N K V V G I I K * W V L G F A L
4081 - TTCCAACAAGCCAACATCTCATAATAATTCTACATGCGTTGATGCATTGTAGAAAATAT - 4140
   -FQQSQHLIIILHALMHCRKY
    S N K A N I S * * F Y M R * C I V E N I
     PTKPTSHNNSTCVDAL*KIY
4141 - ATCAAGGCATAGAGGTACAAAAATTGCGCCTCCTTACCTGCAGCGACAAGCAAAAGATGT - 4200
   - I K A * R Y K N C A S L P A A T S K R C
   - S R H R G T K I A P P Y L Q R Q A K D V
      QGIEVQKLRLLTCSDKQKM*
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4201 - GAATAGATGGTAACAAATAGCAGCAGTAAATTGCAAATGAACTGGAAGCCCTTATAAAGG - 4260
   -E * M V T N S S S K L Q M N W K P L * R
   - N R W * Q I A A V N C K * T G S P Y K G
      I D G N K * Q Q * I A N E L E A L I K G
4261 - GCTAGCTGCCATCTTTTATTGAGCGCAATTATTTTGGTAGCGCTCTGAAAAACAGCAAGA - 4320
   -ASCHLLSAIILVAL * KTAR
   - L A A I F Y * A Q L F W * R S E K Q Q E
      * L P S F I E R N Y F G S A L K N S K K
4321 - AATGCAACGCCAATAACAAGCCATCCGAAAGGGAGTGAGGCTTGTAGCGGTATCGTTGCT - 4380
   -NATPITSHPKGSEACSGIVA
   - M Q R Q * Q A I R K G V R L V A V S L L
      C N A N N K P S E R E * G L * R Y R C C
4381 - GTAGCATGAACAGTACTTGCAGGAGAAGCATTGTCAATTTTTACTGGCTGTGCAGTAATT - 4440
   -VA * T V L A G E A L S I F T G C A V I
      HEQYLQEKHCQFLLAVQ*L
      SMNSTCRRSIVNFYWLCSN*
4441 - GATCCAAGAGTAAAAATCTCATAAACAAATCCATAAGTTCGTTTATGTGTAATGTAATT - 4500
   - D P R V K N L I N K S I S S F M C N V I
     I Q E * K I S * T N P * V R L C V M * F
      S K S K K S H K Q I H K F V Y V * C N L
4501 - TGACACCCTTGAGAACTGGCTCAGAGTCATCCTCATCAAACTTGCAGCAAGAACCACAAG - 4560
   - * H P * E L A Q S H P H Q T C S K N H K
     DTLENWLRVILIKLAARTTR
      T P L R T G S E S S S S N L Q Q E P Q E
4561 - AGCATGCACCCTTGAGGCAACTGCAACAACTAGTCATGCAACAAAGCAAGATTGTAACCA - 4620
   - S M H P * G N C N N * S C N K A R L * P
     A C T L E A T A T T S H A T K Q D C N H
     HAPLRQLQQLVMQQSKIVTM
4621 - TGACGATGGCAATTAGTCCAGCAATGAAGCCGAGCCAAACATACCAAGGCCATTTAATAT - 4680
   - * R W Q L V Q Q * S R A K H T K A I * Y
   - D D G N * S S N E A E P N I P R P F N I
      T M A I S P A M K P S Q T Y Q G H L I Y
4681 - ATTGCTCATATTTTCCCAATTCTTGAAGGTCAATGAGTGATTCATTTAAATTTTTAGCGA - 4740
   -IAHIFPILEGQ*VIHLNF*R
   - L L I F S Q F L K V N E * F I * I F S D
     CSYFPNS*RSMSDSFKFLAT
4741 - CCTCATTGAGGCGGTCAATTTCTTTTTGAATGTTGACGACAGAAGCGTTAATGCCTGAAA - 4800
   -PH * G G Q F L F E C * R Q K R * C L K
   - LIEAVNFFLNVDDRSVNA * N
      S L R R S I S F * M L T T E A L M P E M
4801 - TGTCGCCAAGATCAACATCTGGTGATGTATGATTTTTGAAGTACTTGTCCAGCTCTTCTT - 4860
   -CRQDQHLVMYDF*STCPALL
     VAKINIW * CMIFEVLVQLFF
      SPRSTSGDV*FLKYLSSSSL
4861 - TGAATGAGTCAAGCTCAGGTTGCAGAGGATCATAAACTGTGTTGTTAATGATGCCAATAA - 4920
   - * M S Q A Q V A E D H K L C C * * C Q *
    E * V K L R L Q R I I N C V V N D A N N
      NESSSGCRGS*TVLLMMPIT
4921 - CGACATCACAATTTCCTGAGACAAATGTATTGTCTGTAGTAATTATTTGTGGAGAAAAGA - 4980
   -RHHNFLRQMYCL**LFVEKR
    DITIS * D K C I V C S N Y L W R K E
      T S Q F P E T N V L S V V I I C G E K K
4981 - AGTTCCTCTGTGTAATAAACCAAGAAGTGCCATTAAACACAAAAACACCTTCACGAGGGA - 5040
    - V P L C N K P R S A I K H K N T F T R E
      F L C V I N Q E V P L N T K T P S R G K
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5041 - AGTATGCTTTGCCTTCATGACAAATTGCTGGCGCTGTGGTGAAGTTCCTCTCCTGGGATG - 5100
   -SMLCLHDKLLALW*SSSPGM
   - V C F A F M T N C W R C G E V P L L G W
     Y A L P S * Q I A G A V V K F L S W D G
5101 - GCACATACGTGACATGTAGGAAGACAACACCATGCGGGGCTGCTTGTGGGAAGGACATAA - 5160
   -AHT*HVGRQHHAGLLVGRT*
   - H I R D M * E D N T M R G C L W E G H K
     T Y V T C R K T T P C G A A C G K D I R
5161 - GGTGGTAGCCCTTTCCACAAAAGTCAACTCTTTTTGATTGTCCAAGAACACACTCAGACA - 5220
   -GGSPFHKSQLFLIVQEHTQT
     V V A L S T K V N S F * L S K N T L R H
      W * P F P Q K S T L F D C P R T H S D I
5221 - TTTTAGTAGCAGCAGATTAGCAGAAGCCCTGATTTCAGCAGCCCTGATTAGTTGTTGTG - 5280
   - F * * Q Q D * Q K P * F Q Q P * L V V V
    FSSSKISRSPDFSSPD*LLC
      L V A A R L A E A L I S A A L I S C C V
5281 - TTACATAGGTTTGAAGGCTTTGAAGTCTGCCTGTAATTAACCTGTCAATTTGTACCTCCG - 5340
   -LHRFEGFEVCL*LTCQFVPP
    Y I G L K A L K S A C N * P V N L Y L R
      T * V * R L * S L P V I N L S I C T S A
5341 - CCTCGACTTTATCAAGTCGCGAAAGGATATCATTTAGCACACTTGAAATTGCACCAAAAT - 5400
   -PRLYQVAKGYHLAHLKLHQN
    L D F I K S R K D I I * H T * N C T K I
      STLSSRERISFSTLEIAPKL
5401 - TAGAGCTAAGTTGTTTAACAAGTGTGTTTAATGCTTGAGCATTCTGGTTAACAACGTCTT - 5460
   - * S * V V * Q V C L M L E H S G * Q R L
     RAKLFNKCV * CLSILVNNVL
     ELSCLTSVFNA*AFWLTTSC
5461 - GCAGCTTGCCCAATGCAGTTGATGTTGTTAAGTGATTCTTGAATTTGACTAATCGCCT - 5520
   - A A C P M Q L M L L * V I L E F D * S P
     Q L A Q C S * C C C K * F L N L T N R L
   - SLPNAVDVVSDS*I*LIAL
5521 - TGTTAAATTGGTTGGCGATTTGTTTTTGGTTCTCATAGAGAACATTTTGGGTAACTCCAA - 5580
   -C * I G W R F V F G S H R E H F G * L Q
     V K L V G D L F L V L I E N I L G N S N
     LNWLAICFWFS*RTFWVTPM
5581 - TGCCATTGAACCTATATGCCATTTGCATAGCAAAAGGTATTTGAAGAGCAGCGCCAGCAC - 5640
   -CH * TYMPFA * QKVFEEQRQH
     A I E P I C H L H S K R Y L K S S A S T
      PLNLYAICIAKGI*RAAPAP
5641 - CAAATGTCCATCCAGCAGTGGCAGTACCACTAACTAGAGCAGCAGTGTAGGCAGCAATCA - 5700
   -QMSIQQWQYH*LEQQCRQQS
     K C P S S S G S T T N * S S S V G S N H
      N V H P A V A V P L T R A A V * A A I I
5701 - TATCATCAGTGAGCAGAGGTGGCAACACTGTAAGTCCATTGAACTTCTGCGCACAAATGA - 5760
   - Y H Q * A E V A T L * V H * T S A H K *
     I I S E Q R W Q H C K S I E L L R T N E
      S S V S R G G N T V S P L N F C A Q M R
5761 - GATCTCTAGCATTAATATCACCTAGGCATTCGCCATATTGCTTCATGAAGCCAGCATCAG - 5820
   -DL * H * Y H L G I R H I A S * S Q H Q
     ISSINIT * AFAILLHEASIS
      S L A L I S P R H S P Y C F M K P A S A
5821 - CGAGTGTCACCTTATTAAAGAGCAAGTCCTCAATAAAAGACCTCTTAGTTGGCTTTAGAG - 5880
   -RVSPY*RASPQ*KTS*LALE
   - E C H L I K E Q V L N K R P L S W L * R
      SVTLLKSKSSIKDLLVGFRG
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5881 - GGTCAGGTAATATTTGTGAAAAATTAAAACCACCAAAATATTTCAAAGTTGGGGTTTTGT - 5940
   -GQVIFVKN*NHQNISKLGFC
   - V R * Y L * K I 'K T T K I F Q S W G F V
      SGNICEKLKPPKYFKVGVLY
5941 - ACATTTGTTTGACTTGAGCGAACACTTCACGTGTGTTGCGATCCTGTTCAGCAGCAATAC - 6000
   -TFV * LERTLH V C C D P V Q Q Q Y
   - H L F D L S E H F T C V A I L F S S N T
      ICLT * ANTSRVLRSCSAAIP
6001 - CTGAGAGTGCACGATTTAGTTGTGTGCAAAAGCTACCATATTGGAGAAGCAAATTAGCAC - 6060
   -LRVHDLVVCKSYHIGEAN*H
     * E C T I * L C A K A T I L E K Q I S T
      E S A R F S C V Q K L P Y W R S K L A H
6061 - ATTCAGTAGAATCTCCGCAGATGTACATATTACAATCTACGGAGGTTTTAGCCATAGAAA - 6120
   -IQ*NLRRCTYYNLRRF*P,*K
    F S R I S A D V H I T I Y G G F S H R N
      SVESPQMYILQSTEVLAIET
6121 - CAGGCATTACTTCTGTAGTAATGCTAATTGAAAAGTTAGTAGGTATAGCAATGGTGTTAT - 6180
   - Q A L L L * * C * L K S * * V * Q W C Y
    R H Y F C S N A N * K V S R Y S N G V I
      G I T S V V M L I E K L V G I A M V L L
6181 - TAGAGTAAGCAATTGAACTATCAGCACCTAAAGACATAGTATAAGCCACAATAGATTTTT - 6240
   - * S K Q L N Y Q H L K T * Y K P Q * I F
    R V S N * T I S T * R H S I S H N R F L
     E * A I E L S A P K D I V * A T I D F W
6241 - GGCTAGTACTACGTAATAAAGAAACTGTATGGTAACTAGCACAAATGCCAGCTCCAATAG - 6300
   -G * Y Y V I K K L Y G N * H K C Q L Q *
     A S T T * * R N C M V T S T N A S S N R
     LVLRNKETVW * LAQMPAPIG
6301 - GAATGTCGCACTCATAAGAAGTGTCGACATGCTCAGCTCCTATAAGACAGCCTGCTTGAG - 6360
   -ECRTHKKCRHAQLL*DSLLE
   - N V A L I R S V D M L S S Y K T A C L S
   - MSHS * E V S T C S A P I R Q P A * V
6361 - TCTGGAATACATTGTTTCCAGTAGAATATATGCGCCAAGCTGGTGTGAGTTGATCTGCAT - 6420
   -SGIHCFQ*NICAKLV*VDLH
     - WNTLFPVEYMRQAGVS * SA *
6421 - GAATTGCTGTAGAAACATCAGTGCAGTTAACATCTTGATATAGAACAGCAACTTCAGATG - 6480
   -ELL * K H Q C S * H L D I E Q Q L Q M
   - N C C R N I S A V N I L I * N S N F R *
      I A V E T S V Q L T S * Y R T A T S D E
6481 - AAGCATTTGTTCCAGGTGTAATTACACTTACACCCCCAAAAGAGCAAGGTGAAATGTCTA - 6540
   -KHLFQV*LHLHPQKSKVKCL
   - S I C S R C N Y T Y T P K R A R * N V *
      A F V P G V I T L T P P K E Q G E M S N
6541 - ATATTTCAGATGTTTTAGGATCTCGAACGGAATCAGTGAAATCAGAAACATCACGGCCAA - 6600
   -IFQMF*DLERNQ*NQKHHGQ
     Y F R C F R I S N G I S E I R N I T A K
      I S D V L G S R T E S V K S E T S R P N
6601 - ATTGTTGAAATGGTTGAAATCTCTTTGAAGAAGGAGTTAACACACCAGTACCAGTGAGTC - 6660
   -IVEMVEISLKKELTHQYQ*V
     L L K W L K S L * R R S * H T S T S E S
      \tt C * \tt N G * \tt N L F E E G V N T P V P V S P
6661 - CATTAAAATTAAAATTGACACACTGGTTCTTAATAAGGTCAGTGGATAATTTTGGTCCAC - 6720
   - H * N * N * H T G S * * G Q W I I L V H
   - I K I K I D T L V L N K V S G * F W S T
      LKLKLTHWFLIRSVDNFGPQ
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6721 - AAACCGTGGCCGGTGCATTTAAAAGTTCAAAAGAAAGTACTACAACTCTGTAAGGTTGGT - 6780
   - K P W P V H L K V Q K K V L Q L C K V G
   - N R G R C I * K F K R K Y Y N S V R L V
     T V A G A F K S S K E S T T T L * G W *
6781 - AGCCAATGCCAGTAGTGGTGTAAAAACCATAATCATTTAATGGCCAATAACAATTAAGAG - 6840
   -SQCQ * W C K N H N H L M A N N N * E
   - A N A S S G V K T I I I * W P I T I K S
      PMPVVV*KP*SFNGQ*QLRA
6841 - CAGGTGGGGTGCAAGGTTTGCCATCAGGGGAGAAAGGCACATTAGATATGTCTCTCAA - 6900
   -Q V G C K V C H Q G R K A H * I C L S Q
     R W G A R F A I R G E R H I R Y V S L K
      G G V Q G L P S G E K G T L D M S L S K
6901 - AGGGCCTAAGCTTGCCATGTCTAAGATACCTATATTTATAATTATAATTACCAGTTGAAG - 6960
   -RA*ACHV*DTYIYNYNYQLK
     G P K L A M S K I P I F I I I I T S * S
      G L S L P C L R Y L Y L * L * L P V E V
6961 - TAGCATCAATGTTCCTAGTATTCCAAGCAAGGACACAACCCATGAAATCATCTGGCAATT - 7020
   - * H Q C S * Y S K Q G H N P * N H L A I
     S I N V P S I P S K D T T H E I I W Q F
     A S M F L V F Q A R T Q P M K S S G N L
7021 - TATAATTATAATCAGCAATAACACCAGTTTGTCCTGGCGCTATTTGTCTTACATCATCTC - 7080
    - Y N Y N Q Q * H Q F V L A L F V L H H L
     I I I S N N T S L S W R Y L S Y I I S
       L * S A I T P V C P G A I C L T S S P
7081 - CCTTGACTACAAAGAATCTGCATAGACATTGGAGAAGCAAAGATCATTCAACTTAGTGG - 7140
    - P * L Q K N L H R H W R S K D H S T * W
     LDYKRICIDIGEAKIIQLSG
      L T T K E S A * T L E K Q R S F N L V A
7141 - CAGAAACGCCATAGCACTTAAAGGTTGAAAAAAATGTTGAGTTGTAGAGCACAGAGTAAT - 7200
    -QKRHST*RLKKMLSCRAQSN
     R N A I A L K G * K K C * V V E H R V I
     ETP*HLKVEKNVEL*STE*S
7201 - CAGCAACACAATTAGAAATTTTTTTTCTCTCCCATGCATAGACAGAAGGGAATTTAGTAG - 7260
    -QQHN*KFFFSPMHRQKGI**
     S N T I R N F F S L P C I D R R E F S S
     ATQLEIFFLSHA*TEGNLVA
7261 - CATTAAAAACCTCTCCAAAAGGACACAAGTTTGTAATATTAGGGAATCTCACAACATCTC - 7320
    - H * K P L Q K D T S L * Y * G I S Q H L
     I K N L S K R T Q V C N I R E S H N I S
      LKTSPKGHKFVILGNLTTSP
7321 - CTGAGGGAACAACCCTGAAATTAGAGGTCTGGTAAATTCCTTTGTCAATCTCAAAGCTCT - 7380
    -LREQP * N * R S G K F L C Q S Q S S
      * G N N P E I R G L V N S F V N L K A L
      EGTTLKLEVW*IPLSISKLL
7381 - TAACAGAGCATTTGAGTTCAGCAAGTGGATTTTGAGAACAATCAACAGCATCTGTGATTG - 7440
    - * Q S I * V Q Q V D F E N N Q Q H L * L
     N R A F E F S K W I L R T I N S I C D C
      TEHLSSASGF*EQSTASVIV
7441 - TACCATTTTCATCATACTTGAGCATAAATGTAGTTGGCTTTAAATAGCCAACAAAATAGG - 7500
    - Y H F H H T * A * M * L A L N S Q Q N R
      TIFIILEHKCSWL*IANKIG
      PFSSYLSINVVGFK*PTK*A
7501 - CTGCAGCTGACGTGCCCCAAATGTCTTGAGCAGGTGAAAAGGCTGTAAGAATGGCTCTAA - 7560
    -LQLTCPKCLEQVKRL*EWL*
     C S * R A P N V L S R * K G C K N G S K
      A A D V P Q M S * A G E K A V R M A L K
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7561 - AATTTGTAATGTTAATACCAAGAGGCAACTTAAAAATAGGTTTCAAAGTGTTAAAACCAG - 7620
   - N L * C * Y Q E A T * K * V S K C * N Q
   - I C N V N T K R Q L K N R F Q S V K T R
     FVMLIPRGNLKIGFKVLKPE
7621 - AAGGTAGATCACGAACTACATCTATAGGTTGATAGCCCTTATAAACATAGAGAAACCCAT - 7680
   -KVDHELHL * VDSPYKHRETH
   - R * I T N Y I Y R L I A L I N I E K P I
     G R S R T T S I G * * P L * T * R N P S
7681 - CTTTATTTTTAAACACAAACTCTCGTAAGTGTTTAAAATTACCTGACTTTTCTGAAACAT - 7740
   -LYF*TQTLVSV*NYLTFLKH
     FIFKHKLS * V F K I T * L F * N I
     LFLNTNSRKCLKLPDFSETS
7741 - CAAGCGAAAAGGCATCAGATATGTACTCGAAAGTGCAATTAAATGCATTATCGAATATCA - 7800
   -QAKRHQICTRKCN * MHYRIS
    K R K G I R Y V L E S A I K C I I E Y H
     S E K A S D M Y S K V Q L N A L S N I I
- * Y V S V Y P W V * K Q Q R K G C H T I
    S M C L C T H G F R N S K E R V V T Q F
     V C V C V P M G L E T A K K G L S H N S
7861 - CAAAGTTACATGCTCGTATAACAACATTAGTAGAATTGTTAATAATAATCACCGACTGTG - 7920
   - Q S Y M L V * Q H * * N C * * * S P T V
     K V T C S Y N N I S R I V N N N H R L *
   - KLHARITTLVELLIITDCD
7921 - ACTTGTTGTTCATGGTAGAACCAAAAACCCAACCACGGACAACATTTGATTTCTCTGTGG - 7980
   -TCCSW*NQKPNHGQHLISLW
    L V V H G R T K N P T T D N I * F L C G
     LLFMVEPKTQPRTTFDFSVA
7981 - CAGCAAAATAAATACCATCCTTAAAAGGTATGACAGGGTTGCCAAACGTATGATTAATAG - 8040
   - Q Q N K Y H P * K V * Q G C Q T Y D * *
    SKINTILKRYDRVAKRMINS
    A K * I P S L K G M T G L P N V * L I V
-YETL*H*NKMEEINPELNKE
   - M K P C N I R I K W K K * I L S * I K S
   - * N P V T L E * N G R N K S * V K * R V
8101 - TGTCTGATCTAAAAATTTCATCAGGATAGTAAACCCCCCTCATAGATGAAGTATGTTGAG - 8160
   -CLI * KFHQDSKPPS * MKYVE
   - V * S K N F I R I V N P P H R * S M L S
    S D L K I S S G * * T P L I D E V C * V
8161 - TGTAATTAGGAGCTTGAACATCATCAAAAGTGGTGCACCGGTCAAGGTCACTACCACTAG - 8220
   -CN*ELEHHQKWCTGQGHYH*
    V I R S L N I I K S G A P V K V T T T S
     * L G A * T S S K V V H R S R S L P L V
8221 - TGAGAGTAAGAAATAAGAAAATAAACATGTTCGTTTAGTTGTTAACAAGAATATCAC - 8280
   -* E * E I I R K * T C S F S C * Q E Y H
    ESKK**ENKHVRLVVNKNIT
     R V R N N K K I N M F V * L L T R I S L
8281 - TTGAAACCACAACTCTGTTGTTTTCTCTAATGATAAGCCTACCTTTTTCCAGAAGAGAAT - 8340
   -LKPQLCCFL***AYLFPEEN
      NHNSVVFSNDKPTFQKRI
     ETTTLLFSLMISLPFSRRE*
8341 - AAATCATATCATTGATTTGATTCTCCTTAAGAGACATTACAGCAGTTCCTCTTAATTTAA - 8400
   -KSYH*FDSP*ETLQQFLLI*
    N H I I D L I L L K R H Y S S S S * F K
      IISLI*FSLRDITAVPLNLR
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8401 - GAGGAAATTTGCTCATGTCAAAGAGTGAATAGGAAGACAACTGGATAGGATTTGTGTTCC - 8460
   -EEICSCQRVNRKTTG * D L C S
   - R K F A H V K E * I G R Q L D R I C V P
      G N L L M S K S E * E D N W I G F V F L
8461 - TCCAGAAAATGTAGTTAGCATGCATGGTATAGCCATCAATTTGTTCCTTCGGCTTGCCAA - 8520
   -SRKCS*HAWYSHQFVPSACQ
   - PENVVSMHGIAINLFLRLAK
      Q K M * L A C M V * P S I C S F G L P R
8521 - GATAGTTAGCCCCAATTAAAAATGCTTCCGATGATGATGCATTTACATTTGTAACAAAAG - 8580
   -DS * PQ L K M L P M M M H L H L * Q K
    IVSPN * KCFR * * CIYICN KS
     * L A P I K N A S D D D A F T F V T K A
8581 - CTGTCCACCATGAGAAATGGCCCATAAGCTTGTAAAGGTCAGCATTCCAAGAATGCTCTG - 8640
   -LSTMRNGP*ACKGQHSKNAL
     C P P * E M A H K L V K V S I P R M L C
     V H H E K W P I S L * R S A F Q E C S V
8641 - TTATCTTTACAGCTATAGAACCACCCAGGGCTAGTTTTTGCTTTATAAATCCACACAGAT - 8700
   -LSLQL*NHPGLVFAL*IHTD
     Y L Y S Y R T T Q G * F L L Y K S T Q I
      I F T A I E P P R A S F C F I N P H R *
8701 - AAGTGAAAAACCCTTCTTTAGAGTCATTCTCTTTTGTCACATGTTTGGTCCTAGGGTCAT - 8760
   -K * K T L L * S H S L L S H V W S * G H
     S E K P F F R V I L F C H M F G P R V I
      V K N P S L E S F S F V T C L V L G S Y
8761 - ACATATCGCTAATAATAAGGTCCCATTTATTAGCCGTATGTACTGTTGCACAGTCTCCAA - 8820
   -TYR***GPIY*PYVLLHSLQ
   - H I A N N K V P F I S R M Y C C T V S N
      I S L I I R S H L L A V C T V A Q S P I
8821 - TTAAAGTAGAATCTGCGTCGGAGACGAAGTCATTAAGATCTGAATCGACAAGTAGTGTGC - 8880
    -LK * N L R R R S H * D L N R Q V V C
     * S R I C V G D E V I K I * I D K * C A
     K V E S A S E T K S L R S E S T S S V P
8881 - CAGTTGGCAACCATTGTCTGAGCACAGCTGTACCTGGTGCAACTCCTTTATCAGAGCCAG - 8940
   - Q L A T I V * A Q L Y L V Q L L Y Q S Q - S W Q P L S E H S C T W C N S F I R A S
     V G N H C L S T A V P G A T P L S E P A
-HQSE*LSCCRVQLK*VYLSI
    - T K V N N S H V V G Y S * S K C I * V L
     PK * I T L M L * G T A K V S V F K Y *
9001 - GACACAGTTGAGTATACTTTGCGACATTCATCATTATTCCTTTTGGTATAACAGCATTTT - 9060
    -DTVEYTLRHSSLFLLV*QHF
     T Q L S I L C D I H H Y S F W Y N S I F
      H S * V Y F A T F I I I P F G I T A F S
9061 - CACCATAATTCTGAAGGTCACACTTTTCAAGAAGCATTCTTTGCATCTTGTACAAGTTAG - 9120
    - H H N S E G H T F Q E A F F A S C T S *
     TIILKVTLFKKHSLHLVQVR
        * F * R S H F S R S I L C I L Y K L G
9121 - GCATCGCAACACCTGGTTGCCACGCTTGACTTGCTTGTAGTTTTGGGTAGAAGGTTTCAA - 9180
    -ASQHLVATLDLLVVLGRRFQ
     HRNTWLPRLTCL*FWVEGFN
      I A T P G C H A * L A C S F G * K V S T
9181 - CATGTCCATCCTTACACCAAAGCATGAATGAAATTTCAGCATAGTCAATTGTAACCTTGA - 9240
    - H V H P Y T K A * M K F Q H S Q L * P *
     MSILTPKHE*NFSIVNCNLD
      C P S L H O S M N E I S A * S I V T L T
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9241 - CCACTTTTGAAATCACTGACAAATCTTGTGACTTTATTATCTCGACAAAGTCATCAAGTA - 9300
   -PLLKSLTNLVTLLSRQSHQV
   - H F * N H * Q I L * L Y Y L D K V I K *
      T F E I T D K S C D F I I S T K S S S K
9301 - AAAGATCAATCACAGAACACACATTTTGATGAACCTGTTTGCGCATCTGTTATGAAGT - 9360
   -KDQSQNTHILMNLFAHLL * S
   - KINHRTHTF * * TCLRICYE V
      R S I T E H T H F D E P V C A S V M K *
9361 - AATTTTTCACTGTGCTGTCCATAGGGATAAAATCCTCTAATTTAAGTGGTGAATCTTGTG - 9420
   -NFSLCCP*G*NPLI*VVNLV
    IFHCAVHRDKIL*FKW*IL*
      F F T V L S I G I K S S N L S G E S C E
9421 - AGCGCTTGGCTAAGCCTATCATTAAATGAAGACCGCCAAGTTGTCCATGACTGAAATCTC - 9480
    -SAWLSLSLNEDRQVVHD*NL
     A L G * A Y H * M K T A K L S M T E I S
     R L A K P I I K * R P P S C P * L K S P
9481 - CATAAACGATGTGTTCGAAGGCATAGCCCTCGAGCTTATATCGCTGTATGAATTCATCCA - 9540
    - H K R C V R R H S P R A Y I A V * I H P
     I N D V F E G I A L E L I S L Y E F I H
     * T M C S K A * P S S L Y R C M N S S I
9541 - TAGCGAGCTCGAGAAAGTCAGTTTCCATTTGTGATCTGGGCTTAAAATCCTCTAAGTCTC - 9600
    - * R A R E S Q F P F V I W A * N P L S L
     SELEKVSFHL*SGLKIL*VS
     A S S R K S V S I C D L G L K S S K S L
9601 - TGCTCTGAGTAAAGTAGGTTTCAGGCAACTGTTGAATAATGCCGTCTACTTTCTTAAAGT - 9660
    -CSE*SRFQATVE*CRLLS*S
     A L S K V G F R Q L L N N A V Y F L K V
    - L * V K * V S G N C * I M P S T F L K *
9661 - AGTTAAACTGTGTTTTTACTGATTCTCCAATTAATGTGACTCCATTGACGCTAGCTTGTG - 9720
    - S * T V F L L I L Q L M * L H * R * L V - V K L C F Y * F S N * C D S I D A S L C
    - LNCVFTDSPINVTPLTLACA
9721 - CTGGTCCCTTTGAAGGTGTTAGACCTTTGACTGAACCTTCTGTTATTAAAACACCATTAC - 9780
    - L V P L K V L D L * L N L L L K H H Y
     W S L * R C * T F D * T F C Y * N T I T
    - GPFEGVRPLTEPSVIKTPLR
9781 - GGGCGTTTCTAAAAAGGTCTACCTGTCCTTCCACTCTACCATCAAACAAGACAGTAAGTG - 9840
    -GRF*KGLPVLPLYHQTRQ*V
    - G V S K K V Y L S F H S T I K Q D S K *
      A F L K R S T C P S T L P S N K T V S E
- K N K H S Q * V S W Q C Q S L C R H L L
    - R T S T L S R F L G N V S H C A D T Y C
      E Q A L S V G F L A M S V I V Q T P I V
9901 - TAGATACATGTGCTGGGGCTTCTCTTTTGTAGTCCCAGATTACAGTATTAGCAGCGATAT - 9960
    - * I H V L G L L F C S P R L Q Y * Q R Y
    - R Y M C W G F S F V V P D Y S I S S D I
      D T C A G A S L L * S Q I T V L A A I S
9961 - CAACACCCAAATTATTGAGTATCTTAATCTCTGGCACTGGTTTAATGTTACGCTTAGCCC - 10020
    - N T Q I I E Y L N L W H W F N V T L S P
      T P K L L S I L I S G T G L M L R L A Q
10021 - AAAGCTCAAATGCAACATTAACAGGAAGTGTTGTCTTATTTTCAAAGATCTCCACATCAA - 10080
    -KAQMQH*QEVLSYFQRSPHQ
    - K L K C N I N R K C C L I F K D L H I N
      S S N A T L T G S V V L F S K I S T S I
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10081 - TACCATCTACCTTTGTGTAAACAGCATTATTAATGATGGAAACAGGTGCTTCGCCGGCGT - 10140
   -YHLPLCKQHY**WKQVLRRR
   - TIYLCVNSIINDGNRCFAGV
     PSTFV*TALLMMETGASPAC
10141 - GTCCATCAAAGTGTCCTTTATTAACAACATTATAAGCCACATTTTCTAAACTCTGTAACC - 10200
    -VHQSVLY*QHYKPHFLNSVT
   - SIKVSFINNIISHIF * TL * P
     PSKCPLLTTL * ATFSKLCNL
-W * M Y S T G Y K Y Q I V C K S I G * I
     G K C I P Q V I S I K L F V N P * A K S
      V N V F H R L * V S N C L * I H R L N P
10261 - CAGCAGAAATCATCATATTATATGCATCCAAGTACTGTCGGTACTCATTTGCATGGTGTC - 10320
    -QQKSSYYMHPSTVGTHLHGV
     S R N H H I I C I Q V L S V L I C M V S
      A E I I I L Y A S K Y C R Y S F A W C L
10321 - TGCAAACAGCACCACCTAAATTGCATCGTGTAATACACGTAGCAGATTTGAGTGGAACAT - 10380
    -CKQHHLNCIV*YT*QI*VEH
     A N S T T * I A S C N T R S R F E W N I
     QTAPPKLHRVIHVADLSGT *
10381 - AATCAATATCCGACACTACTTGTTTGCCATGAGACTCACAAGGACTATCAGAATAGTAAA - 10440
    -NQYPTLLVCHETHKDYQNSK
    - INIRHYLFAMRLTRTIRIVK
      SISDTTCLP*DSQGLSE**K
10441 - AGAAAGGCAATTGCTTTAAATTAGTAAATGCACTTTTATCGAAAGCTGGAGTGTGGAATG - 10500
    - R K A I A L N * * M H F Y R K L E C G M
    - ERQLL*ISKCTFIESWSVEC
      K G N C F K L V N A L L S K A G V W N A
10501 - CATGCTTATTCACATACAAACTACCACCATCACAGCCTGGTAAGTTCAAGTTTGACAAGA - 10560
    C L F T Y K L P P S Q P G K F K F D K T
10561 - CTCTTGTGTCAAACCTACACACAATTGCATTGGCTGGGTAACGATCAACGTTACAATTCC - 10620
    -LLCQTYTQLHWLGNDQRYNS
    - S C V K P T H N C I G W V T I N V T I P
     L V S N L H T I A L A G * R S T L Q F Q
10621 - AAAACAAACAACACCATCAGTGAATTTATCGTGATGTGTAGCATAAGAATAGAAGAGTT - 10680
    -KTNKHHQ*IYRDV*HKNRRV
    - K Q T N T I S E F I V M C S I R I E E F
      N K Q T P S V N L S * C V A * E * K S S
10681 - CCTCTATTTTGTAAGCTTTGTCACTACATGGCTGAGCATCGTAGAACTTCCATTCTACTT - 10740
    - P L F C K L C H Y M A E H R R T S I L L
    - L Y F V S F V T T W L S I V E L P F Y F
      SIL*ALSLHG*AS*NFHSTS
10741 - CAGCCTGAGGCACACTTGATAGCCTTTGGATTTCCAATGTCATGAAGAACTGGAAACT - 10800
    -QPEAHT**PLDFQCHEELET
      S L R H T L D S L W I S N V M K N W K L
      A * G T H L I A F G F P M S * R T G N L
10801 - TATCAGCAAGCAATGCAGACTTCACAACCATGTGTTGTACTTTTCTGCAAGCAGAATTAA - 10860
    -YQQAMQTSQPCVVLFCKQN*
      I S K Q C R L H N H V L Y F S A S R I N
      S A S N A D F T T M C C T F L Q A E L T
10861 - CCCTCAGTTCATCTCCTATAATAGGGTATTCAACAGACCAATCAACGCGCTTAACAAAGC - 10920
    -PSVHLL**GIQQTNQRA*QS
     P Q F I S Y N R V · F N R P I N A L N K A
      L S S S P I I G Y S T D Q S T R L T K H
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10921 - ACTCATGGACTGCTAAACATCTAGTCATGATAGCATCACAACTAGCCACATGTGCATTTC - 10980
    - L M D C * T S S H D S I T T S H M C I S
       S W T A K H L V M I A S Q L A T C A F P
10981 - CATGTACCTGGCAATGTTGGTCATGGTTACTCTGAAGGTTACCCGTAAAGCCCCACTGCT - 11040
    - H V P G N V G H G Y S E G Y P * S P T A
    - MYLAMLVMVTLKVTRKAPLL
       CTWQCWSWLL*RLPVKPHC*
11041 - GAACATCAATCATAAATGGGTTATAGACATAGTCAAAACCCACAGAATGATTCCAGCAGG - 11100
    -EHQS*MGYRHSQNPQNDSSR
     NINHKWVIDIVKTHRMIPAG
       TSIINGL * T * S K P T E * F Q Q A
11101 - CATAAGTATCTGATGAAGTAGAAAAGCAAGTTGCACGTTTGTCACACAGACAACACGTTC - 11160
    - H K Y L M K * K S K L H V C H T D N T F
     ISI**SRKASCTFVTQTTRS
      * V S D E V E K Q V A R L S H R Q H V L
11161 - TTTCAGGTCCAATCTTGACAAAGTACTTCATTGATGTAAGCTCAAAGCCATGCGCCCAAA - 11220
    -FQVQS*QSTSLM*AQSHAPK
     FRSNLDKVLH * CKLKAMRPK
       S G P I L T K Y F I D V S S K P C A Q R
11221 - GGACGAACACGACTCTGTCTGACAATCCTTTCAGTGTATCACTGAGCATTTGTACTATCT - 11280
    -GRTRLCLTILSVYH*AFVLS
    - D E H D S V * Q S F Q C I T E H L Y Y L
       T N T T L S D N P F S V S L S I C T I L
11281 - TAATACGCACTACATTCCAGGGCAAGCCTTTATACATGAGTGGTATAAGATGTTTAAACT - 11340
    - * Y A L H S R A S L Y T * V V * D V * T
      N T H Y I P G Q A F I H E W Y K M F K L
       I R T T F Q G K P L Y M S G I R C L N W
11341 - GGTCACCTGGTGGAGGTTTTGCATTAACTCTGGTGAATTCTGTGTTATTTTCAGTGTCAA - 11400
    -GHLVEVLH*LW*ILCYFQCQ
      V T W W R F C I N S G E F C V I F S V N
       S P G G G F A L T L V N S V L F S V S T
11401 - CATAACCAGTCGGTACAGCTACTAAGTTAACACCTGTAGAAAATCCTAGCTGGAGAGGTA - 11460
    - H N Q S V Q L L S * H L * K I L A G E V
    - I T S R Y S Y * V N T C R K S * L E R *
      * P V G T A T K L T P V E N P S W R G R
11461 - GGTTAGTACCCACAGCATCTCTAGTTGCATGACAGCCCTCTACATCAAAGCCAATCCACG - 11520
    -G * Y P Q H L * L H D S P L H Q S Q S T
- V S T H S I S S C M T A L Y I K A N P R
      L V P T A S L V A * Q P S T S K P I H A
11521 - CACGAACGTGACGAATAGCTTCTTCGCGGGTGATAAACATATTAGGGTAACCATTGACTT - 11580
    - H E R D E * L L R G * * T Y * G N H * L
     - T N V T N S F F A G D K H I R V T I D L
       R T * R I A S S R V I N I L G * P L T W
11581 - GGTAATTCATTTTGAAACCCATCATAGAGATGAGTCTACGGTAGGTCATGTCCTTTGGTA - 11640
     -GNSF*NPS*R*VYGRSCPLV
      V I H F E T H H R D E S T V G H V L W Y
       * FILKPIIEMSLR * V M S F G M
11641 - TGCCTGGTATGTCAACACATAATCCTTCAGTCTTGAATTTTATATCAACGCTGAGGTGTG - 11700
     -CLVCQHIILQS*ILYQR*GV
-AWYVNT*SFSLEFYINAEVC
       PGMSTHNPSVLNFISTLRCV
11701 - TAGGTGCCTGTGTAGGATGAAGACCAGTAATGATCTTACTACAGTCCTTAAAAAAGTCCAG - 11760
     - * V P V * D E D Q * * S Y Y S P * K V Q
     - R C L C R M K T S N D L T T V L K K S S
       G A C V G * R P V M I L L Q S L K S P V
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11761 - TTACATTTTCTGCTTGTAATGTAGCCACATTGCGACGTGGTATTTCTAGACTTGTAAATT - 11820
    -LHFLLVM*PHCDVVFLDL*I
    - Y I F C L * C S H I A T W Y F * T C K L
      T F S A C N V A T L R R G I S R L V N C
11821 - GCAGTTTGTCATAAAGATCTCTATCAGACATTATGCACAAAATGCCAATTTTTGCCCTTG - 11880
    - A V C H K D L Y Q T L C T K C Q F L P L
    - Q F V I K I S I R H Y A Q N A N F C P C
      S L S * R S L S D I M H K M P I F A L V
11881 - TGATAGCCACATTGAAGCGGTTGACATTACAAGAGTGTGCTGTTTCAGTAGTTTGTGTGA - 11940
    - * * P H * S G * H Y K S V L F Q * F V *
    - D S H I E A V D I T R V C C F S S L C E
     IATLKRLTLQECAVSVVCVN
11941 - ATATGACATAGTCATATTCAGAACCCTGTGATGAATCAACAGTCTGCGTAGGCAATCCTA - 12000
    -I * H S H I Q N P V M N Q Q S A * A I L
     Y D I V I F R T L * * I N S L R R Q S *
       M T * S Y S E P C D E S T V C V G N P K
12001 - AGATTTTTGAAGCTACAGCGTTCTGTGAATTATAAGGTGAGATAAAAACAGCTTTTCTCC - 12060
    -RFLKLQRSVNYKVR * KQLFS
    - D F * S Y S V L * I I R * D K N S F S P
       I F E A T A F C E L * G E I K T A F L Q
12061 - AAGCAGGATTGCGTGTAAGAAATTCTCTTACAACGCCTATTTGAGGTCTGTTGATTGCAG - 12120
    -KQDCV*EILLQRLFEVC*LQ
    - S R I A C K K F S Y N A Y L R S V D C R
       AGLRVRNSLTTPI*GLLIAD
12121 - ATGAAACATCATGTGTAATAACACCTTTGTAGAACATTTTGAAGCATTGAGCTGACTTAT - 12180
    - M K H H V * * H L C R T F * S I E L T Y
      * N I M C N N T F V E H F E A L S * L I
      ETSCVITPL*NILKH*ADLS
12181 - CCTTGTGTGCTTTTAGCTTATTGTCATAAACTAAAGCACTCACAGTGTCAACAATTTCAG - 12240
    -PCVLLAYCHKLKHSQCQFQ
    - L V C F * L I V I N * S T H S V N N F S
       L C A F S L L S * T K A L T V S T I S A
12241 - CAGGACAACGGCGACAAGTTCCAAGGAACATGTCTGGACCTATTGTTTTCATAAGTCTGC - 12300
    -QDNGDKFQGTCLDLLFS*VC
      RTTATSSKEHVWTYCFHKSA
      G Q R R Q V P R N M S G P I V F I S L H
12301 - ACACTGAATTAAAATATTCTGGTTCTAGTGTGCCTTTAGTCAGCAATGTGCGGGGGGCTG - 12360
    -TLN*NILVLVCL*SAMCGGL
    - H * I K I F W F * C A F S Q Q C A G G W
       T E L K Y S G S S V P L V S N V R G A G
12361 - GTAATTGAGCAGGATCGCCAATATAGACGTAGTGTTTTGCACGAAGTCTAGCATTGACAA - 12420
     -VIEQDRQYRRSVLHEV*H*Q
       * L S R I A N I D V V F C T K S S I D N
       N * A G S P I * T * C F A R S L A L T T
12421 - CACTCAAGTCATAATTAGTAGCCATAGAGATTTCATCAAAGACTACAATGTCAGCAGTTG - 12480
     - H S S H N * * P * R F H Q R L Q C Q Q L
      TQVIISSHRDFIKDYNVSSC
       L K S * L V A I E I S S K T T M S A V V
12481 - TTTCTGGCAATGCATTTACAGTGCAGAAAACATACTGTTCTAGTGTTGAATTCACTTTGA - 12540
     -FLAMHLQCRKHTVLVLNSL*
      FWQCIYSAENILF*C*IHFE
       S G N A F T V Q K T Y C S S V E F T L N
12541 - ATTTATCAAAACACTCTACGCGCGCACGCGCAGGTATGATTCTACTACATTTATCTATGG - 12600
     -IYQNTLRAHAQV*FYYIYLW
      F I K T L Y A R T R R Y D S T T F I Y G
       LSKHSTRARAGMILLHLSMG
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12601 - GCAAATATTTTAATGCCTTTTCACATAGGGCATCAACAGCTGCATGAGAGCATGCCGTAT - 12660
    -ANILMPFHIGHQQLHESMPY
    - Q I F * C L F T * G I N S C M R A C R I
       K Y F N A F S H R A S T A A * E H A V Y
12661 - ACACTATGCGAGCAGATGGGTAATAGAGAGCAAGTCCGATGGCAAAATGACTCTTACCAG - 12720
    -TLCEQMGNREQVRWQNDSYQ
    - H Y A S R W V I E S K S D G K M T L T S
       T M R A D G * * R A S P M A K * L L P V
12721 - TACCAGGTGGTCCTTGGAGTGTAGAGTACTTTTGCATGCCGACCTTTTGATAATTTGCAA - 12780
    -YQVVLGV*STFACRPFDNLQ
      TRWSLECRVLLHADLLIICN
       P G G P W S V E Y F C M P T F * * F A T
12781 - CATTGCTAGAAAACTCATCTGAGATGTTGAGTGTTGGGTACAAGCCAGTAATTCTCACAT - 12840
     -HC*KTHLRC*VLGTSQ*FSH
     I A R K L I * D V E C W V Q A S N S H I
       LLENSSEMLSVGYKPVILT *
12841 - AGTGCTCTTGTGGCACTAGAGTAGGTGCACTAAGTGGCATTACAGTGTGAGATGTCAACA - 12900
     -SALVALE * VH * VALQCEMST
      V L L W H * S R C T K W H Y S V R C Q H
       C S C G T R V G A L S G I T V * D V N T
12901 - CAAAGTAATCACCAACATTCAACTTGTATGTCGTAGTACCTCTGTACACAACAGCATCAC - 12960
     -QSNHQHSTCMS*YLCTQQHH
      K V I T N I Q L V C R S T S V H N S I T
      K * S P T F N L Y V V P L Y T T A S P
12961 - CATAGTCACCTTTTTCAAAGGTGTACTCTCCAATCTGTACTTTACTATTTTTAGTTACAC - 13020
     - H S H L F Q R C T L Q S V L Y Y F * L H
     - I V T F F K G V L S N L Y F T I F S Y T
       * S P F S K V Y S P I C T L L F L V T R
13021 - GGTAACCAGTAAAGACATAGTTTCTGTTCAATGGTGGTCTAGGTTTTCCAACCTCCCATG - 13080
     - G N Q * R H S F C S M V V * V F Q P P M
     - V T S K D I V S V Q W W S R F S N L P *
       * P V K T * F L F N G G L G F P T S H E
13081 - AAAGATGCAATTCTCTGTCAGAGAGTACTTCGCGTACAGTGGCAATACCATATGACAGCT - 13140
     -KDAILCQRVLRVQWQYHMTA
     - K M Q F S V R E Y F A Y S G N T I * Q L
       R C N S L S E S T S R T V A I P Y D S L
13141 - TAAATGTTTCCTCAGTGGCTTTGAGCGTTTCTGCTGCGAAAAGCTTGAGTCTCTCAGTAC - 13200
     - * M F P Q W L * A F L L R K A * V S Q Y
- K C F L S G F E R F C C E K L E S L S T
        N V S S V A L S V S A A K S L S L S V Q
13201 - AAGTGTTGGCAAGTATGTAATCGCCAGCATTAGTCCAATCACATGTTGCTATCGCATTGA - 13260
     - K C W Q V C N R Q H * S N H M L L S H *
- S V G K Y V I A S I S P I T C C Y R I E
        V L A S M * S P A L V Q S H V A I A L K
13261 - AGTCAGTGACATTGTCACTGCCTACACATGTGTTTTTGTATAAACCAAAAACCTGACCAT - 13320
     -SQ * H C H C L H M C F C I N Q K P D H
       V S D I V T A Y T C V F V * T K N L T I
        S V T L S L P T H V F L Y K P K T * P L
13321 - TAGCACATAATGGAAAACTAATGGGAGGCTTATGTGACTTGCAATAATAGCTCATACCTC - 13380
     - * H I M E N * W E A Y V T C N N S S Y L
       S T * W K T N G R L M * L A I I A H T S
A H N G K L M G G L C D L Q * * L I P P
13381 - CTAGATACAGTTGTCACATCAGTGACATCACAACCTGGGGCATTGCAAACATAGGGAT - 13440
     - L D T V V S H Q * Н Н N L G Н С К Н R D
       * I Q L C H I S D I T T W G I A N I G I
        R Y S C V T S V T S Q P G A L Q T * G L
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13441 - TAACAGACAACACTAATTTGTGTGATGTTGAAATGACATGGTCATAGCAGCACTTGCAAC - 13500
    - * Q T T L I C V M L K * H G H S S T C N
    - N R Q H * F V * C * N D M V I A A L A T
      T D N T N L C D V E M T W S * Q H L Q H
13501 - ATAGGAATGGTCTCCTAATACAGGCACCGCAACGAAGTGAAGTCTGTGAATTGCACAATA - 13560
    -IGMVS*YRHRNEVKSVNCTI
    - * E W S P N T G T A T K * S L * I A Q Y
      R N G L L I Q A P Q R S E V C E L H N T
13561 - CACAAGCACCTACAGCCTGCAAGACTGTATGTGGTGTACATAGCCTCATAAAACTCAG - 13620
    - H K H L Q P A R L Y V V C T * P H K T Q
      T S T Y S L Q D C M W C V H S L I K L R
      Q A P T A C K T V C G V Y I A S * N S G
13621 - GTTCCCAGTACCGTGAGGTGTTATCATTAGTTAGCATTACGGAATACATGTCCAACATGT - 13680
    -VPSTVRCYH*LALRNTCPTC
     FPVP*GVIIS*HYGIHVQHV
      S Q Y R E V L S L V S I T E Y M S N M W
13681 - GGCCAGTAAGCTCATCATGTAACTTTCTAATGTATTGTAAATACAAGTGAAAGACATCAG - 13740
    -GQ * A H H V T F * C I V N T S E R H Q
     ASKLIM*LSNVL*IQVKDIS
      P V S S S C N F L M Y C K Y K * K T S A
13741 - CATACTCCTGATTAGGATGTTTTGTAAGTGGGTAAGCATCAATAGCCAGTGACACGAACC - 13800
    - H T P D * D V L * V G K H Q * P V T R T
     I L L I R M F C K W V S I N S Q * H E P
      YS*LGCFVSG*ASIASDTNL
13801 - TTTCAATCATAAGTGTACCATCTGTTTTGACAATATCATCGACAAAACAGCCTGCGCCTA - 13860
    -FQS*VYHLF*QYHRQNSLRL
     FNHKCTICFDNIIDKTACA*
      SIISVPSVLTISSTKQPAPN
13861 - ATATTCTTGATGGATCTGGGTAAGGCAGGTACACGTAATCATCTCCTTGTTTAACTAGCA - 13920
    -IFLMDLGKAGTRNHLLV*LA
      Y S * W I W V R Q V H V I I S L F N * H
       I L D G S G * G R Y T * S S P C L T S I
13921 - TTGTATGCTGTGAGCAAAATTCGTGAGGTCCTTTAGTAAGGTCAGTCTCAGTCCAACATT - 13980
    -LYAVSKIREVL**GQSQSNI
    - C M L * A K F V R S F S K V S L S P T F
      V C C E Q N S * G P L V R S V S V Q H F
13981 - TTGCCTCAGACATGAACACATTATTTTGATAATAAAGAACTGCCTTAAAGTTCTTAATGC - 14040
    -LPQT*THYFDNKELP*SS*C
    - CLRHEHIILIKNCLKVLNA
       ASDMNTLF**RTALKFLML
14041 - TAGCTACTAAACCTTGAGCCGCATAGTTACTGTTATAGCACACCACCGCATCATCAGAAA - 14100
    - * L L N L E P H S Y C Y S T Q R H H Q K
- S Y * T L S R I V T V I A H N G I I R K
       ATKP*AA*LLL*HTTASSER
14101 - GAATCATCATGGAGAAATGTTTACGCAGGTAAGCGTAAAACTCATCCACGAATTCATGAT - 14160
    -ESSWRNVYAGKRKTHPRIHD
    - N H H G E M F T Q V S V K L I H E F M I
       I I M E K C L R R * A * N S S T N S * S
14161 - CAACATCCCTATTTCTATAGAGACACTCATAGAGCCTGTGTTGTAGATTGCGGACATACT - 14220
    -Q H P Y F Y R D T H R A C V V D C G H T
      N I P I S I E T L I E P V L * I A D I L
       T S L F L * R H S * S L C C R L R T Y L
14221 - TGTCAGCTATCTTATTACCATCAGTTGAAAGAAGTGCATTTACATTGGCTGTAACAGCTT - 14280
    -CQLSYYHQLKEVHLHWL*QL
     - V S Y L I T I S * K K C I Y I G C N S L
       SAILLPSVERSAFTLAVTA *
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14281 - GACAAATGTTAAAGACACTATTAGCATAAGCAGTTGTAGCATCACCGGATGATGTTCCAC - 14340
    - D K C * R H Y * H K Q L * H H R M M F H
    - TNVKDTISISSCSITG * CST
       Q M L K T L L A * A V V A S P D D V P P
14341 - CTGGTTTAACATATAGTGAGCCGCCACACATGACCATCTCACTTAATACTTGCGCACACT - 14400
    -LV * HIVSRHT * PSHLILAHT
    - W F N I * * A A T H D H L T * Y L R T L
       G L T Y S E P P H M T I S L N T C A H S
14401 - CGTTAGCTAACCTGTAGAAACGGTGTGATAAGTTACAGCAAGTGTTATGTTTGCGAGCAA - 14460
    -R * L T C R N G V I S Y S K C Y V C E Q
     VS*PVETV**VTASVMFASK
       L A N L * K R C D K L Q Q V L C L R A R
14461 - GAACAAGAGAGGCCATTATCCTAAGCATGTTAGGCATGGCTCTGTCACATTTTGGATAAT - 14520
    -EQERPLS * A C * A W L C H I L D N
    - N K R G H Y P K H V R H G S V T F W I I
       TREAILS MLG MALS HFG * S
14521 - CCCAACCCATAAGGTGTGGAGTTTCTACATCACTGTAAACAGTTTTTAACATATTATGCC - 14580
    - P N P * G V E F L H H C K Q F L T Y Y A
      PTHKVWSFYITVNSF*HIMP
       O P I R C G V S T S L * T V F N I L C Q
14581 - AGCCACCGTAAAACTTGCTTGTTCCAATTACCACAGTAGCTCCTCTAGTGGCGGCTATTG - 14640
    -SHRKTCLFQLPQ*LL*WRLL
      ATVKLACSNYHSSSSGGY*
      PP * N L L V P I T T V A P L V A A I D
14641 - ACTTCAATAATTTCTGATGAAACTGTCTATTTGTCATAGTACTACAGATAGAGACACCAG - 14700
     -TSIISDETVYLS*YYR*RHQ
      LQ * FLMKLSICHSTTDRDTS
        F N N F * * N C L F V I V L Q I E T P A
14701 - CTACGGTGCGAGCTCTATTCTTTGCACTAATGGCATACTTAAGATTCATTTGAGTTATAG - 14760
    -LRCELYSLH*WHT*DSFEL*
      Y G A S S I L C T N G I L K I H L S Y S
      TVRALFFALMAYLRFI*VIV
14761 - TAGGGATGACATTACGCTTAGTATACGCGAAAAGTGCATCTTGATCCTCATAACTCATTG - 14820
    - * G * H Y A * Y T R K V H L D P H N S L
- R D D I T L S I R E K C I L I L I T H *
      G M T L R L V Y A K S A S * S S * L I E
14821 - AGTCATAATAAAGTCTAGCCTTACCCCATTTATTAAATGGGAAACCAGCTGATTTATCCA - 14880
     -SHNKV*PYPIY*MGNQLIYP
     - VIIKSSLTPFIKWETS*FIQ
        S * * S L A L P H L L N G K P A D L S R
14881 - GATTGTTAACGATTACTTGGTTGGCATTAATACAGCCACCATCGTAACAATCAAAGTATT - 14940
     -DC * RLLGWH * YSHHRNNQSI
       I V N D Y L V G I N T A T I V T I K V F
        L L T I T W L A L I Q P P S * Q S K Y L
14941 - TATCAACAACTTCAACTACGAATAGGAGTTGTCTGATATCACACATTGTTGGCAGATTAT - 15000
     -YQQLQLRIGVV*YHTLLADY
        \hbox{\tt I} \quad \hbox{\tt N} \quad \hbox{\tt N} \quad \hbox{\tt F} \quad \hbox{\tt N} \quad \hbox{\tt Y} \quad \hbox{\tt E} \quad \hbox{\tt *} \quad \hbox{\tt E} \quad \hbox{\tt L} \quad \hbox{\tt S} \quad \hbox{\tt D} \quad \hbox{\tt I} \quad \hbox{\tt T} \quad \hbox{\tt H} \quad \hbox{\tt C} \quad \hbox{\tt W} \quad \hbox{\tt Q} \quad \hbox{\tt I} \quad \hbox{\tt I} 
      STTSTTNRSCLISHIVGRL*
15001 - AACGATAATAGTCATAATCACTGATAGCAGCGTTGCCATCCTGAGCAAAGAAGAAGTGTT - 15060
     -NDNSHNH**QRCHPEQRRSV
     - TIIVIITDSSVAILSKEEVF
     - R * * S * S L I A A L P S * A K K C F
15061 - TTAGTTCAACAGAACTTCCTTCCTTAAAGAAACCTTTAGACACAGCAAAGTCATAAAAGT - 15120
     -L V Q Q N F L P * R N L * T Q Q S H K S
       * FNRTSFLKETFRHSKVIKV
        S S T E L P S L K K P L D T A K S * K S
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-LY*NYRV*QFEKQHCLLVQL
    - FIKITGFDSLKSNIVC * CSY
      LLKLPGLTV * KATLFVSAAT
-LKSM * CVYLAINCQKLHA * L
      * K A C S A F I * Q * I A R S C M H S W
       E K H V V R L S S N K L P E A A C I A G
15241 - GATCAGCAGCATACACTAAAAGTTCCTTGAAACTGAGACGCGAGCTATGTAAGTTTACAT - 15300
    -DQQHTLKVP*N*DASYVSLH
    - I S S I H * K F L E T E T R A M * V Y I
       S. A A Y T K S S L K L R R E L C K F T S
15301 - CCTGATTATGTACGACTCCTAACTCACGAAAATGGTATCCAGTTGAAACAACAAAAGGAA - 15360
    - P D Y V R L L T H E N G I Q L K Q Q K E
      L I M Y D S * L T K M V S S * N N K R N
       * L C T T P N S R K W Y P V E T T K G T
15361 - CACCATCTACAAATATTTTTCTTACTAGTGGTCCAAAACTTGTAGGTGGAAACACAGTAG - 15420
    - H H L Q I F F L L V V Q N L * V E T Q *
      T I Y K Y F S Y * W S K T C R W K H S R
       P S T N I F L T S G P K L V G G N T V E
15421 - AAAATAACACATTAAAGTTTGCACAATGAAGGATACACCTATCATCCAAACAGTTAATAC - 15480
     -KITH * SLHNEGYTYHPNS * Y
     K * H I K V C T M K D T P I I Q T V N T
      N N T L K F A Q * R I H L S S K Q L I Q
15481 - AATTGGGATGGTATGTCTGGTCCCAATATTTAAAATAACGGTCGAAGAGACAAAGTCTCT - 15540
    -NWDGMSGPNI*NNGRRDKVS
      I G M V C L V P I F K I T V E E T K S L
     - LGWYVWSQYLK*RSKRQSLS
15541 - CTTCCGTAAAATCATATTTCAGCAAATCCCACTTAATAAGTGGTTTTGCGAGATCAGCAT - 15600
     -LP*NHISANPT**VVLRDQH
    - FRKIIFQQIPLNKWFCEISI
       S V K S Y F S K S H L I S G F A R S A S
15601 - CCATATGGGACTCAGCAGCCAATGCCCTAGTCAAAGTGAGGATGGGCATCAGCAATGAGT - 15660
    - P Y G T Q P M P * S K * G W A S A M S
     - H M G L S S Q C P S Q S E D G H Q Q * V
      I W D S A A N A L V K V R M G I S N E *
15661 - AATATGAATCCACAATAGGAACTCCGCAGCCTGGTGCTACTTGTACGAAATCACCGAAAT - 15720
     -NMNPQ*ELRSLVLLVRNHRN
     - I * I H N R N S A A W C Y L Y E I T E I
      Y E S T I G T P Q P G A T C T K S P K S
15721 - CGTACCAGTTCCCATTAAGATCCTGATTATCTAATGTCAGTACGCCTACAATGCCTGCAT - 15780
     -RTSSH*DPDYLMSVRLQCLH
     - V P V P I K I L I I * C Q Y A Y N A C I
       Y Q F P L R S * L S N V S T P T M P A S
15781 - CACGCATAGCATCGCAGAATTGTACAGTCTTTAATAATGATTGGCGTACACGCTCACCTA - 15840
     - H A * H R R I V Q S L I M I G V H A H L
     - T H S I A E L Y S L * * * L A Y T L T *
       R I A S Q N C T V F N N D W R T R S P K
15841 - AGTTAGCATATACGCGTAAGATGTCAGGATTCTCTACGAAGTCATACCAATCCTTCTTAT - 15900
     -S * H I R V R C Q D S L R S H T N P S Y
      V S I Y A * D V R I L Y E V I P I L L I
       L A Y T R K M S G F S T K S Y Q S F L L
15901 - TGAAATAATCATCACAGCAATTGTATGTGACGAGTATTTCTTTTAATGTATCACAAT - 15960
     - * N N H H H S N C M * R V F L L M Y H N
     - E I I I T A I V C D E Y F F * C I T I
        \texttt{K} \;\; \star \;\; \texttt{S} \;\; \texttt{S} \;\; \texttt{Q} \;\; \texttt{Q} \;\; \texttt{L} \;\; \texttt{Y} \;\; \texttt{V} \;\; \texttt{T} \;\; \texttt{S} \;\; \texttt{I} \;\; \texttt{S} \;\; \texttt{F} \;\; \texttt{N} \;\; \texttt{V} \;\; \texttt{S} \;\; \texttt{Q} \;\; \texttt{L}
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- Y P H Q N D V E H R L N Q P L C I * L D
    - TLIKMT * SID * I SHC V F S * T
      PSSK*RRA*TKSAIVYLVRR
16021 - GCTGACGTGATATATGTGGTACCATGTCACCATCTACTCTAAACTTGAAAAAGTCATGGA - 16080
    - A D V I Y V V P C H H L L * T * K S H G
    - L T * Y M W Y H V T I Y S K L E K V M D
      * R D I C G T M S P S T L N L K K S W T
16081 - CAGCAACCGCTGGACAATCTTTAACCAAGTTATAAATAGTCTCTTCATGTTGGTAGTTAG - 16140
    -QQPLDNL*PSYK*SLHVGS*
    - S N R W T I F N Q V I N S L F M L V V R
      ATAGQSLTKL*IVSSCW*LD
16141 - ACATAGTATGCCTCTTAACTACAAAGTAAGAGTCTAATAAATTGCCTTCCTCATCCTTCT - 16200
    -T * Y A S * L Q S K S L I N C L P H P S
    - H S M P L N Y K V R V * * I A F L I L L
      I V C L L T T K * E S N K L P S S S F S
16201 - CCTGGAAGCGACAGCAATTAGTTTTTAGGAACTTTGCAAAACCAGCACTTTTTTCGTTGT - 16260
    - P G S D S N * F L G T L Q N Q H F F R C
     LEATAISF*ELCKTSTFFVV
      W K R Q Q L V F R N F A K P A L F S L *
16261 - AAATATCAAAAGCCCTGTAGACGACATCAGTACTAGTGCCTGTGCCGCACGGTGTAAGAC - 16320
    -KYQKPCRRHQY*CLCRTV*D
    - N I K S P V D D I S T S A C A A R C K T
      I S K A L * T T S V L V P V P H G V R R
16321 - GGGCTGCACTTACACCGCAAACCCGTTTAAAAACGTTGATGCATCCGCAGACTGCATCAA - 16380
    -GLHLHRKPV*KR*CIRRLHQ
      G C T Y T A N P F K N V D A S A D C I K
      A A L T P Q T R L K T L M H P Q T A S R
16381 - GGGTTCGCGGAGTTGGTCACAACTACAGCCATAACCTTTCCACATTCCGCAGACGGTACA - 16440
    -GFAELVTTTAITFPHSADGT
      G S R S W S Q L Q P * P F H I P Q T V Q
      V R G V G H N Y S H N L S T F R R R Y R
-DCVSKCKTHWVISTSGRYLD
      T V F L S V K P T G S L A Q V V G I W T
      L C F * V * N P L G H * H K W * V F G R
16501 - GTACTTACCTTTCAAGTCACAGAATCCTTTAGGATTTGGATGGTCAATGTGGCATCTACA - 16560
    -VLTFQVTESFRIWMVNVAST
      Y L P F K S Q N P L G F G W S M W H L Q
       TYLSSHRIL*DLDGQCGIYN
16561 - ATACAGACAACATGAAGCACCACCAAAGGACTCTTGGTCCATGTTAGCTTCTGGTGTTAC - 16620
    -IQTT * STTKGLLVHVSFWCY
      Y R Q H E A P P K D S W S M L A S G V T
       T D N M K H H Q R T L G P C * L L V L Q
16621 - AGTAATTGCCTGTCCTGTACCAGTGTGTGTACACACATCTTCACACAGTTGGTGATTGG - 16680
    -SNCLSCTSVCTQHLHTVGDW
      V I A C P V P V C V H N I F T Q L V I G
       * L P V L Y Q C V Y T T S S H S W * L V
16681 - TTGTCCTCCACTTGCTAGGTAATCCTTATATGCTTTAGCAGGGTCTACTGCAAAAGCACA - 16740
     -LSSTC*VILICFSRVYCKST
      C P P L A R * S L Y A L A G S T A K A Q
       V L H L L G N P Y M L * Q G L L Q K H R
16741 - GAAGGAAAGCACAGTTGAATTGGCAGGTACTTCTGTAGCATTTCCAGCCTGAAGACGTAC - 16800
     - E G K H S * I G R Y F C S I S S L K T Y
- K E S T V E L A G T S V A F P A * R R T
       R K A Q L N W Q V L L * H F Q P E D V L
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16801 - TGTAGCAGCTAAACTGCCCAGCACCATACCTCTATTTAGGTTGTTTAAGCCTTTGATGAA - 16860
    -CSS*TAQHHTSI*VV*AFDE
    - V A A K L P S T I P L F R L F K P L M K
- * Q L N C P A P Y L Y L G C L S L * * S
16861 - GTACAAGTATTTCACTTTAGGCCCTTTTGGTGTGTCTGTAACAAACCTACAAGGTGGTTC - 16920
    -VQVFHFRPFWCVCNKPTRWF
    - Y K Y F T L G P F G V S V T N L Q G G S
       TSISL * ALL V C L * Q T Y K V V P
16921 - CAGTTCTGTGTAAATTGTACCTGTACCATCACTCTTAGGGAATCTAGCCCATTTGAGATC - 16980
    -QFCVNCTCTITLRESSPFEI
     SSV * I V P V P S L L G N L A H L R S
       V L C K L Y L Y H H S * G I * P I * D L
16981 - TTGGTGGTCTGATAGTAATGCCAGCACAAACCTACCTCCCTTCGAATTGTTATAGTAGGC - 17040
    -LVV***CQHKPTSLRIVIVG
     W W S D S N A S T N L P P F E L L * * A
       G G L I V M P A Q T Y L P S N C Y S R Q
17041 - AAGTGCATTGTCATCAGTACAAGCTGTTTGTGTGGGTACCAGCCGCACAGGACATCTGTCG - 17100
    - K C I V I S T S C L C G T S R T G H L S
      S A L S S V Q A V C V V P A A Q D I C R
      V H C H Q Y K L F V W Y Q P H R T S V V
17101 - TAGTGCTACTGGACTCAGTTCATTATTCTGTAGTTTAACAGCTGAGTTGGCTCTTAGAGC - 17160
     - * C Y W T Q F I I L * F N S * V G S * S
      S A T G L S S L F C S L T A E L A L R A
       V L L D S V H Y S V V * Q L S W L L E L
17161 - TGTAACAATAAGAGGCCAAGCCAAATTTGGTGAATTGTCCATGTTAATTTCACTAAGTTG - 17220
    -CNNKRPSQIW*IVHVNFTKL
      V T I R G Q A K F G E L S M L I S L S *
       * Q * E A K P N L V N C P C * F H * V E
17221 - AACAATCTTGCTATCCGCATCAACAACTTGCTGGATTTCCCAGAGTGCAGATGCATATGT - 17280
     -NNLAIRINNLLDFPECRCIC
      TILLSASTTCWISQSADAYV
       OSCYPHQQLAGFPRVQMHM*
17281 - AAAGGTGTTACCATCACAAGTGTTCTTGTAGGTACCATAATCAGGGACAACAACCATGAG - 17340
    -KGVTITSVLVGTIIRDNNHE
     - K V L P S Q V F L * V P * S G T T T M S
      RCYHHKCSCRYHNQGQQP*V
17341 - TTTGGCTGCTGTAGTCAATGGTATGATGTTGAGTGGAACACCATCACGCGCATTGTT - 17400
    -FGCCSQWYDVEWNTTITRIV
-LAAVVNGMMLSGTQPSRALL
-WLL*SMV*C*VEHNHHAHC*
17401 - GATAATGTTGTTAAGTGCATCATTATCAAGCTTCCTAAGCATAGTGAAGAGCATTGTTTG - 17460
     -DNVVKCIIIKLPKHSEEHCL
       I M L L S A S L S S F L S I V K S I V C
       * C C * V H H Y Q A S * A * * R A L F A
17461 - CATAGCACTAGTTACTTTTGCCCTCTTGTCCTCAGATCTTGCCTGTTTTGTACATTTGGGT - 17520
     - H S T S Y F C P L V L R S C L F V H L G
       I A L V T F A L L S S D L A C L Y I W V
       * H * L L P S C P Q I L P V C T F G S
17521 - CATAGCCTGATCTGCCATCTTTTCCAACTTGCGTTGCATGGCAGCATCACGGTCAAACTC - 17580
     - H S L I C H L F Q L A L H G S I T V K L
       I A * S A I F S N L R C M A A S R S N S
       * PDLPSFPTCVAWQHHGQTQ
17581 - AGATTTAGCCACATTCAAAGATTTCTTTAACTTTTTGAGAACGACTTCAGAATCACCATT - 17640
     -RFSHIQRFL*LFENDFRITI
     - D L A T F K D F F N F L R T T S E S P L
        I * P H S K I S L T F * E R L Q N H H *
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17641 - AGCTACAGCCTGCTCATAGGCCTCCTGGGCAGTGGCATAAGCGGCATATGATGGTAAAGA - 17700
    -SYSLLIGLLGSGISGI * W * R
    - A T A C S * A S W A V A * A A Y D G K E
      LQPAHRPPGQWHKRHMMVKN
17701 - ACTAAATTCTGAAGCAATAGCCTGAAGAGTAGCACGGTTATCGAGCATTTCCTCGCACAA - 17760
    -TKF * SNSLKSSTVIEHFLAQ
    - L N S E A I A * R V A R L S S I S S H N
       * I L K Q * P E E * H G Y R A F P R T T
17761 - CCTATTAATGTCTACAGCACCCTGCATGGATAGCAAAACAGACAAAAGAGAAACCATCTT - 17820
    -PINVYSTLHG * QNRQKRNHL
     L L M S T A P C M D S K T D K R E T I F
       Y * C L Q H P A W I A K Q T K E K P S S
17821 - CTCGAAAGCTTCAGTTGTGTCTTTTGCAAGAAGAATATCATTGTGGAGTTGTACACATTG - 17880
    -LESFSCVFCKKNIIVELYTL
      S K A S V V S F A R R I S L W S C T H C
       R K L Q L C L L Q E E Y H C G V V H I V
17881 - TGCCCACAATTTAGAAGATGACTCTACTCTAAGTTGTTGAAGAACCGAGAGCAGTACCAC - 17940
    -CPQFRR*LYSKLLKNREQYH
     A H N L E D D S T L S C * R T E S S T T
      PTI*KMTLL*VVEEPRAVPQ
17941 - AGATGTGCACTTTACGTCAGACATTTTAGACTGTACAGTAGCAACCTTGATACATGGTTT - 18000
    -RCALYVRHFRLYSSNLDTWF
    - D V H F T S D I L D C T V A T L I H G L
    - M C T L R Q T F * T V Q * Q P * Y M V Y
18001 - ACCTCCAATACCCAACAACTTAATGTTAAGCTTGAAAGCATCAATACTACTCTTAGGAGG - 18060
    -TSNTQQLNVKLESINTTLRR
      P P I P N N L M L S L K A S I L L L G G
       L Q Y P T T * C * A * K H Q Y Y S * E A
18061 - CAAAAGCCCCTGGGAGTTCATATACCTAAATTCTTGTGTAGAGACCAAGTAGTCATAAAC - 18120
    -Q K P L G V H I P K F L C R D Q V V I N
      K S P W E F I Y L N S C V E T K * S * T
       KAPGSSYT*ILV*RPSSHKH
18121 - ACCAAGAGTAAGCCTGAAGTAACGGTTGAGTAAACAGAAAAGGCCAAAGTAGCAGCAGCA - 18180
    -TKSKPEVTVE * TEKAKVAAA
    - PRVSLK*RLSKQKRPK*QQQ
      QE * A * S N G * V N R K G Q S S S N
18181 - ACAATAGCCTAAGAAACAATAAACAAGCATGATACACTGTAAGGTGTTGCCAGTAATAAA - 18240
    - T I A * E T I N K H D T L * G V A S N K
- Q * P K K Q * T S M I H C K V L P V I N
       N S L R N N K Q A * Y T V R C C Q * * I
18241 - TAACAATGGGTAATACTCAACACACACAAACACTATAGCTCTAGCTAAAAACATGATAGT - 18300
     - * Q W V I L N T H K H Y S S S * K H D S
     - N N G * Y S T H T N T I A L A K N M I V
       T M G N T Q H T Q T L * L * L K T * * S
18301 - CGTAACGACACCAGAATAGTTAGAGGTTACAGAAATAACTAAGGCCCACATGGAAATAGC - 18360
     -RNDTRIVRGYRNN*GPHGNS
      V T T P E * L E V T E I T K A H M E I A
       * R H Q N S * R L Q K * L R P T W K * L
18361 - TTGATCTAAAGCATTACCATAGTAGACTTTGTAAACAAGTGTAATGACATTCATCAGTGT - 18420
     -LI*SITIVDFVNKCNDIHQC
       SKALP**TL*TSVMTFISV
       D L K H Y H S R L C K Q V * * H S S V S
18421 - CCAAACACGTCTAGCAGCATCATCATAAACAGTGCGAGCTGTCATGAGAATAAGCAAAAC - 18480
     - P N T S S S I I I N S A S C H E N K Q N
       Q T R L A A S S * T V R A V M R I S K T
       KHV * Q H H H K Q C E L S * E * A K L
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18481 - TAAAGCTGAAGCATACATAACACAATCCTTAAGCCTATAACCAGACAAGCTAGTGTCAGC - 18540
    - * S * S I H N T I L K P I T R Q A S V S
    - KAEAYITQSLSL*PDKLVSA
      K L K H T * H N P * A Y N Q T S * C Q P
18541 - CAATTCAAGCCATGTCATGATACGCATCACCCAGCTAGCAGGCATGTAGACCATATTAAA - 18600
    -QFKPCHDTHHPASRHVDHIK
    - NSSHVMIRITQLAGM*TILK
       I Q A M S * Y A S P S * Q A C R P Y * S
18601 - GTAAGCAACTGTTGCAAGAGAAGGTAACAGAAACAAGCACAAGAATGCGTGCTTATGCTT - 18660
    - V S N C C K R R * Q K Q A Q E C V L M L
      * A T V A R E G N R N K H K N A C L C L
       KQLLQEKVTETSTRMRAYA*
18661 - AACAAGCAGCATAGCACATGCAGCAATTGCCATAATACCAAGAGTAAATGGCAAGAAAGC - 18720
    -N K Q H S T C S N C H N T K S K W Q E S
     T S S I A H A A I A I I P R V N G K K A
       Q A A * H M Q Q L P * Y Q E * M A R K H
18721 - ATTCTCGTAAACAAAGAAAACAGTGACCACTGTGTACTTTGAACAAGAATCAATAGTGA - 18780
    -ILVNKEKQ*PLCTLNKNQ**
     FS*TKKNSDHCVL*TRINSD
       S R K Q R K T V T T V Y F E Q E S I V M
18781 - TGTCAAGAAAGTTAAAAGCATCCAATGATGAGTGCCCTTAACAATTTTCTTGAACTTACC - 18840
    -CQES*KHPMMSALNNFLELT
     V K K V K S I Q * * V P L T I F L N L P
       S R K L K A S N D E C P * Q F S * T Y L
18841 - TTGGAAGGTAACACCAGAGCATTGTCTAACAACATCAAATGGTGTAAACTCATCTTCTAA - 18900
    -LEGNTRALSNNIKWCKLIF *
      W K V T P E H C L T T S N G V N S S S K
      GR*HQSIV*QHQMV*THLLK
18901 - AATAGTGCTACCAAGGATAGTACGACCATTCATACCATTCTGCAGCAGCTCTTTCAAAGC - 18960
    -NSATKDSTTIHTILQQLFQS
      I V L P R I V R P F I P F C S S S F K A
       * C Y O G * Y D H S Y H S A A A L S K Q
18961 - AGCACACATATCTAAGACGGCAATTCCTGTTTGAGCAGAAAGAGGTCCCAATATGTCAAC - 19020
    -STHI*DGNSCLSRKRSQYVN
-AHISKTAIPV*AERGPNMST
      H T Y L R R Q F L F E Q K E V P I C Q H
19021 - ATGATCTTGTGTCAAAGGTTCATAGTTGTACTTCATTGCCACAAGGTTAAAGTCATTCAA - 19080
    - M I L C Q R F I V V L H C H K V K V I Q
- * S C V K G S * L Y F I A T R L K S F K
    - DLVSKVHSCTSLPQG*SHSK
19081 - AGTAGTGGTGAATCTATTAAGAAACCACCTATCACCATTGATAACAGCAGCATACAGCCA - 19140
    -SSGESIKKPPITIDNSSIQP
    - V V V N L L R N H L S P L I T A A Y S H
    - * W * I Y * E T T Y H H * * Q Q H T A M
-CQNI*CYGCVCTCSLSV
    - A K T F N V M V V S V P A A C A V C L S
      P K H L M L W L C L Y L Q P V Q F V C Q
19201 - AACAAATGGACCATAGAATTTACCTTCTAAGTCAGTACCAGCGTGTACTCCTGTTGGAAG - 19260
    -NKWTIEFTF * VSTSVYSCWK
    - T N G P * N L P S K S V P A C T P V G S
       Q M D H R I Y L L S Q Y Q R V L L E A
19261 - CTCCATATGATGCATATAGCAGAAAGACACGCAATCATAATCAATGTTAAAACCAACACT - 19320
    - L H M M H I A E R H A I I I N V K T N T
- S I * C I * Q K D T Q S * S M L K P T L
       P Y D A Y S R K T R N H N Q C * N Q H Y
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19321 - ACCACATGATCCATTAAGGAAAGAACCTTTAATGGTATGATTAGGTCTCATGGCACACTG - 19380
   -TT*SIKERTFNGMIRSHGTL
   - P H D P L R K E P L M V * L G L M A H *
      H M I H * G K N L * W Y D * V S W H T D
19381 - ATAAACACCAGATGGTGAACCATTGTAGCATGCTAGAACTGAAAATGTTTGACCAGGTTG - 19440
   -INTRW*TIVAC*N*KCLTRL
    * T P D G E P L * H A R T E N V * P G W
      K H Q M V N H C S M L E L K M F D Q V G
19441 - GATACGGACAAATTTATACTTGGGTGTCTTAGGGTTAGAAGTATCAACTTTAAGCCTAAG - 19500
   -DTDKFILGCLRVRSINFKPK
    I R T N L Y L G V L G L E V S T L S L S
      Y G Q I Y T W V S * G * K Y Q L * A * A
19501 - CAGACAATTTTGCATAGAATGGCCAATAACACGAAGTTGAACATTGCCAGCCTGAACAAG - 19560
   -QTILHRMANNTKLNIASLNK
    R Q F C I E W P I T R S * T L P A * T R
      D N F A * N G Q * H E V E H C Q P E Q E
19561 - AAAGCTATGGTTGGATTTGCGAATGAGCAGATCTTCATAGTTAGGATTAAGCATGTCTTC - 19620
    -KAMVGFANEQIFIVRIKHVF
   - KLWLDLRMSRSS * LGLSMSS
      SYGWICE * ADLHS * D * ACLL
19621 - TGCTGTGCAAATGACATGTCTTGGACAGTATACTGTGTCATCCAACCACAATCCATTAAG - 19680
    -CCANDMSWTVYCVIQPQSIK
     A V Q M T C L G Q Y T V S S N H N P L R
     LCK*HVLDSILCHPTTIH*E
19681 - AGTTGTAGTTCCACAGGTTACTTGTACCATGCACCCTTCAACTTTGCCTGACGGGAATGC - 19740
    -SCSSTGYLYHAPFNFA*REC
     V V P Q V T C T M H P S T L P D G N A
      L * F H R L L V P C T L Q L C L T G M P
-HFPKTTLQNSRSD*CLWWLV
     IFLKPLCRTAEVIDVCGGW*
      FS*NHSAEQQK*LMSVVVGR
19801 - GAGAACATCAGCACCTGAGTTGCTAAAGTCATTTAGAGCCTTTGCTAAGTGGCAGCAAGC - 19860
    -ENIST * VAKVI * SLC * VAAS
    - R T S A P E L L K S F R A F A K W Q Q A
    - EHQHLSC*SHLEPLLSGSKL
19861 - TGCTTCACGATAGCTGGTAGTATCTAAGGCTCCACTGAAATACTTGTACTTGTTATATAG - 19920
    -CFTIAGSI*GSTEILVLVI*
     ASR*LVVSKAPLKYLYLLYR
    - L H D S W * Y L R L H * N T C T C Y I E
19921 - AGCAAGATACCTGTTATACTGTGTAAGTGGCAACAGTGTCTCGCTACGCAATTTTAGGTA - 19980
    -SKIPVILCKWQQCLATQF*V
-ARYLLYCVSGNSVSLRNFRY
    - QDTCYTV * VATVSRYAILGT
19981 - CATTTCCTTGTTGAGCAAAAAGGTACACAAAGCAGCCTCCTCGAAGGTACTAAATGTAAC - 20040
    - H F L V E Q K G T Q S S L L E G T K C N
     I S L L S K K V H K A A S S K V L N V T
     FPC*AKRYTKQPPRRY*M*L
20041 - TCCATTAAACATGACTCTTTTCCTAAGATAGTTGTTAAAGAACCAATGGCAGTGCTTCAG - 20100
    -SIKHDSFPKIVVKEPMAVLQ
      PLNMTLFLR*LLKNQWQCFR
     H * T * L F S * D S C * R T N G S A S E
20101 - AGAAATACAGAATACATAGATTGCTGTTATCCAAAAAGGCACAATAGGAGAAAACATGGC - 20160
    -RNTEYIDCCYPKRHNRRKHG
    - EIQNT*IAVIQKGTIGENMA
      KYRIHRLLSKKAQ * EKTWQ
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20161 - AAACCATTGAAGGTGAGCCAAGAATGAAACATCATTGGTGAAATAGAATGTCAAGTACAA - 20220
    - K P L K V S Q E * N I I G E I E C Q V Q
    - N H * R * A K N E T S L V K * N V K Y K
      T I E G E P R M K H H W * N R M S S T S
-V K D * V D S R Q K A V S W Y Q T E Y S
     * K T E * T P G R K L * A G T R Q S I V
      K R L S R L P A E S C K L V P D R V * *
20281 - GAAAGACATCAAAAACAAAAGTGCATTAGCAGCAACAACATGGTTGTACTCACCAAAAAC - 20340
    -ERHQKQKCISSNNMVVLTKN
     K D I K N K S A L A A T T W L Y S P K T
      K T S K T K V H * Q Q Q H G C T H Q K H
20341 - ACGTCTGAATTTCATAAAGTAGTAGGCAGCACAAGTCACCAATATGGCAATAATACCACC - 20400
    -TSEFHKVVGSTSHQYGNNTT
     RLNFIK**AAQVTNMAIIPP
      V * I S * S S R Q H K S P I W Q * Y H Q
20401 - AGCCACTACTGAAGCAGACATCTAAAGCACCCACAGGTTGCACAAGAGGAGTAAAGAT - 20460
    -SHY*SRHI*STHRLHKRSKD
     A T T E A D T S K A P T G C T R G V K M
     PLLKQTHLKHPQVAQEE*RC
20461 - GTTAGCTATGAGATTCATCGCATCAACACCACAGAAAACTCCTGATAGAGCTCTGTAATG - 20520
    -VSYEIHRINTTENS**SSVM
     LAMRFIASTPQKTPDRAL * C
     * L * D S S H Q H H R K L L I E L C N A
20521 - CTCATTATTAAGAACCCATCTACCACTGGTAGATAGGCAAATACCTACTTCTGACCTTTC - 20580
    -LIIKNPSTTGR*ANTYF*PF
      S L L R T H L P L V D R Q I P T S D L S
     HY*EPIYHW*IGKYLLLTFR
20581 - GCATGTACCATGTCTACAGTACTCAGCATCAAAAGTTGTTACTACTCTAACAGAACCCTC - 20640
    - A C T M S T V L S I K S C Y Y S N R T L
    - H V P C L Q Y S A S K V V T T L T E P S
    - MYHVYSTQHQKLLLL*QNPP
20641 - CAGGTAAGTGTTAGGAAACTGTATGATGGAACCATCCATAAGCACATAACGAGTGTCTGG - 20700
    - Q V S V R K L Y D G T I H K H I T S V W
- R * V L G N C M M E P S I S T * R V S G
    - G K C * E T V * W N H P * A H N E C L D
20701 - ACGAAGCTCACTATAAGAAATAGAACCCTCTAGCAAATTAGTGTCATAACAATATGGCAC - 20760
    -TKLTIRNRTL*QISVITIWH
-RSSL*EIEPSSKLVS*QYGT
      E A H Y K K * N P L A N * C H N N M A Q
20761 - AGGTTTGCCCATAGCATCCTTAAAAATTGTACACTCAGCAGCAAGAACGCAAGCAGAGGT - 20820
    -RFAHSILKNCTLSSKNASRG
    - G L P I A S L K I V H S A A R T Q A E V
      V C P * H P * K L Y T Q Q E R K Q R *
20821 - AGCAAAATCACTATACTCAATGAGTTTGGAAGGTGTGTAGCAAATGTTGCCAACAGCACT - 20880
    -SKITILNEFGRCVANVANST
    - A K S L Y S M S L E G V * Q M L P T A L
       Q N H Y T Q * V W K V C S K C C Q Q H *
-KNTR * KMQEVTIDCSQHSTR
    - KTRGRKCKKSPLIALSTVPG
       K H E V E N A R S H H * L L S A Q Y P V
20941 - TAAGCCAGGCACTATGAAACCAATCTCTCTTGTAATGATAGCAGCTACTACAGGGCAGCT - 21000
    - * A R H Y E T N L S C N D S S Y Y R A A
    - K P G T M K P I S L V M I A A T T G Q L
       SQAL*NQSLL***QLLQGSF
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21001 - TTTGTCATTTTTGTATGAACCACCACGCTGGCTAAACCATGCGTCAAAACCAGCATGTTT - 21060
    -FVIFV*TTTLAKPCVKTSMF
    - L S F L Y E P P R W L N H A S K P A C L
     CHFCMNHHAG*TMRQNQHVY
21061 - ATTTGCAAAACAATCATCAGTAGAAATGATGTCACGAGTGACACCATCCTGAATGGCTTT - 21120
    -ICKTIISRNDVTSDTILNGF
     FAKQSSVEMMSRVTPS*MAL
      L Q N N H Q * K * C H E * H H P E W L C
-V T N D F I C V T I M D * Q C M Y W H N
       PMISFV * PSWIDNVCTGIT
      NQ * F H L C N H H G L T M Y V L A * R
21181 - GATATAACAAACCAATGCAGCAAGAACGCACAATAATGTGGCCTTAAGCATAAGTTTAAA - 21240
    -DITNQCSKNAQ*CGLKHKFK
     I * Q T N A A R T H N N V A L S I S L K
     YNKPMQQERTIMWP*A*V*N
21241 - ACAAGTACTAACAATCTTACCACCCTTGAGTGAGATTTTAGTAGTATTATGACATTGACAAC - 21300
    -TSTNNLTTLE * DFSSYDIDN
      Q V L T I L P P L S E I L V V M T L T T
      K Y * Q S Y H P * V R F * * L * H * Q P
21301 - CTGTCTAGTTGTAGCACAAGTTAGTGTAAAAGGTATGTTGTTCTTCTTGGCAGCAGTACG - 21360
    -LSSCSTS * CKRYVVLLGSST
      C L V V A Q V S V K G M L F F L A A V R
     V * L * H K L V * K V C C S S W Q Q Y E
21361 - AATTTGTTTACGCAGCTGTTCAGATAAAGACATGTAGTCTTTTACATTCCAGATGAGTGA - 21420
    -NLFTQLFR*RHVVFYIPDE*
    - I C L R S C S D K D M * S F T F Q M S E
      F V Y A A V Q I K T C S L L H S R * V K
21421 - AACATTGTGACTTTTTGCTACTTGGGCATTGATATGCCTTGCATTACAGTCAATACATGC - 21480
    -NIVTFCYLGIDMPCITVNTC
-TL*LFATWALICLALQSIHA
      HCDFLLLGH*YALHYSQYMR
21481 - GCCAAGATCTCTGGGCGTCATGTTTTCAACCTTATTATAGGTGAGCATGAAATTGTTACA - 21540
    - A K I S G R H V F N L I I G E H E I V T
    - PRSLGVMFSTLL * VSMKLLQ
    - Q D L W A S C F Q P Y Y R * A * N C Y N
21541 - ACTGTCACCTGTCACTTCTAAGTCAGAGTGATGTGAAAGTTTGAGACATTCAATAACATC - 21600
    -TVTCHF*VRVM*KFETFNNI
    - L S P V T S K S E * C E S L R H S I T S
       C H L S L L S Q S D V K V * D I Q * H P
21601 - CTTTGTGTCAACATCGGTATCAACAACACCTTGTCGGGCAGCTGACACGAATGTAGAAAG - 21660
    -LCVNIGINNTLSGS*HECRK
    - F V S T S V S T T P C R A A D T N V E R
       L C Q H R Y Q Q H L V G Q L T R M * K G
21661 - GACACCATCTAAAGCTACACCCTTTGCTAACTCGCTGTGAGCTGTAGCAACAAGTGCCTT - 21720
    -DTI*SYTLC*LAVSCSNKCL
    - T P S K A T P F A N S L * A V A T S A L
       H H L K L H P L L T R C E L * Q Q V P *
21721 - AAGTTTTTCCATAGGAACACTAAAAGTTGCTGAAAAGGTGTCGACATAAGCATCAAACAT - 21780
    -KFFHRNTKSC * KGVDISIKH
    - S F S I G T L K V A E K V S T * A S N I
       V F P * E H * K L L K R C R H K H Q T S
21781 - CTTAACGGAAACTTCAGTACTATCTCCAACGTTTGATACAAGAGCTTGGTCAAGCAACAG - 21840
    -LNGNFSTISNV*YKSLVKQQ
    - L T E T S V L S P T F D T R A W S S N R
       * R K L Q Y Y L Q R L I Q E L G Q A T E
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21841 - AATAGGTTGGCACATCAGCTGACTGTAGTACACAGAAGCAGACTTAGAAGCAGACTCGTC - 21900
    -NRLAHQLTVVHRSRLRSRLV
    - I G W H I S * L * Y T E A D L E A D S S
       * V G T S A D C S T Q K Q T * K Q T R R
21901 - GCATTTGGACTTGCCATCAAAAACTATGACATTAATAGGCAGTGAACCTTTAGTGTTGTT - 21960
    - A F G L A I K N Y D I N R Q * T F S V V
    - H L D L P S K T M T L I G S E P L V L L
       I W T C H Q K L * H * * A V N L * C C *
21961 - AGCTCTCAAATTGTCTAAATTGACAAAATGGGAGAGCGGATGTCTCTCATAGGTCTTTTG - 22020
    -SSQIV*IDKMGERMSLIGLL
    - A L K L S K L T K W E S G C L S * V F *
    - LSNCLN * QNGRADVSHRSFD
22021 - ACCAGCCTTGTCAAAGTAGAGGTGAAGCGCGCCATTTTTCACAGCAACACTATCAACAAT - 22080
    -TSLVKVEVKRAIFHSNTINN
     PALSK*R*SAPFFTATLSTI
       Q P C Q S R G E A R H F S Q Q H Y Q Q Y
22081 - ATACGATGACTGGTCAGTAGGGTTGATTGGTCTTTTAAACTGGAGTGACAAATCACGAGC - 22140
     -IR * L V S R V D W S F K L E * Q I T S
      Y D D W S V G L I G L L N W S D K S R A
       T M T G Q * G * L V F * T G V T N H E Q
22141 - AACTTCATCACTAATGAATGTACTACCAGTGCAAAATGTGTCACAATTGAGACAATTCCA - 22200
     -N F I T N E C T T S A K C V T I E T I P
      T S S L M N V L P V Q N V S Q L R Q F Q
       L H H * * M Y Y Q C K M C H N * D N S N
22201 - ATTGTGAGTCTTGCAGAAGCCACGGCCTCCATTTGCATAGACATAGAAAGATCTCTTCAT - 22260
     -IVSLAEATASICIDIERSLH
      L * V L Q K P R P P F A * T * K D L F M
       C E S C R S H G L H L H R H R K I S S C
22261 - GCCATTAACAATAGTTGTACACTCAACGCGTGTGGCACGATTGCGCTTATAGCACATCAT - 22320
     - A I N N S C T L N A C G T I A L I A H H
      P L T I V V H S T R V A R L R L * H I M
      H * Q * L Y T Q R V W H D C A Y S T S C
22321 - GCAAGTCGAAGAGGTGCAACCATCCATGATATGAACATAGCTCTTCCATATGTAGTAGAA - 22380
     - A S R R G A T I H D M N I A L P Y V V E
      Q V E E V Q P S M I * T * L F H M * * K
      K S K R C N H P * Y E H S S S I C S R K
22381 - AGAAGCAAAGAAGATGTACATCCTAACCATTGCAGAAACGGGTGCCATTTGTACAATACT - 22440
     -RSKEDVHPNHCRNGCHLYNT
     - E A K K M Y I L T I A E T G A I C T I L
       K Q R R C T S * P L Q K R V P F V Q Y *
22441 - AATGATAAACCACATGAGCCAAGAATTGCTGATGAAATGACTAGCAAAAATAGCCAAAGAA - 22500
     -NDKPHEPRIADEMTSKIAKE
     - M I N H M S Q E L L M K * L A K * P K N
       * * T T * A K N C * * N D * Q N S Q R T
22501 - CACCTGCATTATAGCTGAAAGACCTAATAAATAAAAGAATTTTGTGAACAACATATATGC - 22560
     - H L H Y S * K T * * I K E F C E Q H I C
     - TCIIAERPNK * KNFVNNIYA
        PAL*LKDLINKRIL*TTYMP
22561 - CAAAACCCACTCAGCGGCCAGACCTAAAATTGTCAAGTCTAGCTTGTACGATGAAATCGT - 22620
     - Q N P L S G Q T * N C Q V * L V R * N R
     - K T H S A A R P K I V K S S L Y D E I V
      K P T Q R P D L K L S S L A C T M K S S
22621 - CACCTGAATGGTTTCAAGAGCTGGATAAGAATCAAGGGAGTCTAATCCACTTAAACAAAT - 22680
     - H L N G F K S W I R I K G V * S T * T N
- T * M V S R A G * E S R E S N P L K Q M
        P E W F Q E L D K N Q G S L I H L N K C
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22681 - GCTGCAAGGAAAGAACCTTCACAGAAATCCATAGTAGTAACGTTAGACGAATTAAGATA - 22740
    - A A R K R T F T E I H S S N V R R I K I
    - L Q G K E P S Q K S I V V T L D E L R Y
     C K E K N L H R N P * * * R * T N * D T
22741 - CAATTCTCTAACGCCATTACAATAAGAAGGAGCACCAAAATTAGATAAGAGTACACCAAA - 22800
    -QFSNAITIRRSTKIR*EYTK
    - N S L T P L Q * E G A P K L D K S T P K
      I L * R H Y N K K E H Q N * I R V H Q K
22801 - AGCAGCAGTTACACAGATTAGAGAACCTAAGCAAATACTTAACAACAATAGCCACATAGC - 22860
    -SSSYTD*RT*ANT*QQ*PHS
     A A V T Q I R E P K Q I L N N N S H I A
      Q Q L H R L E N L S K Y L T T I A T * R
-DCEQFRKFG*LHIINAGIQT
     I V N N L E N L G D F T * L M P A S K H
     L * T I * K I W V T S H N * C R H P N I
-* F S N T L N T I F S N S C R * * S S N
     N L A T L L T L F L A I V V G S E A L I
      I * Q H S * H Y F * Q * L * V V K L * F
22981 - TCTAGAATTGGTACTTTTAGTAAAAGTACACAATTGGAACAATAATGTAAACACATAAGG - 23040
    -SRIGTFSKSTQLEQ*CKHIR
     LELVLLVKVHNWNNNVNT * G
      * N W Y F * * K Y T I G T I M * T H K A
23041 - CATATAATTGTTAAACACACGTTGTGCTAATCTCTTAGCGCAATTTGATGTTGTAATTGC - 23100
    -HIIVKHTLC * SLSAI * CCNC
    - I * L L N T R C A N L L A Q F D V V I A
      YNC * THVVLIS * RNLML * LL
23101 - TGCTTGTCCTAAGAATGGTTTGACATAAGCCAAAATTTTACTCCAAGGAACACTATTAAT - 23160
    -CLS*EWFDISQNFTPRNTIN
    - A C P K N G L T * A K I L L Q G T L L I
      L V L R M V * H K P K F Y S K E H Y * L
23161 - TGCAGCAATACCATGAGTGGCAATTGTTTTTAAACCTAAGGCTAGTGAAAGCTCATTAGG - 23220
    - C S N T M S G N C F * T * G * * K L I R
    - A A I P * V A I V F K P K A S E S S L G
      Q Q Y H E W Q L F L N L R L V K A H * V
23221 - TTTCTTAATGGTAATGCTTGTGTTTTCCACATAAGCAGCCATAAGATCCTCATGACCTAA - 23280
    -FLNGNACVFHISSHKILMT*
    - F L M V M L V F S T * A A I R S S * P N
      S * W * C L C F P H K Q P * D P H D L T
23281 - CTCTTGTGTTACTTTAACACCTTCATCTGATGGTTTAAGTATGACATTGCCTACAACTTC - 23340
    - L L C Y F N T F I * W F K Y D I A Y N F
- S C V T L T P S S D G L S M T L P T T S
       L V L L * H L H L M V * V * H C L Q L R
23341 - GGTAGTTTTCACGTCACACTCTATGACTTCCTTCTGTATGGTAGGATTTTCCACTACTTC - 23400
    -GSFHVTLYDFLLYGRIFHYF
      V V F T S H S M T S F C M V G F S T T S
       * F S R H T L * L P S V W * D F P L L L
23401 - TTCAGAGGTGGGTTGTTGACTTTCACAAGCAAGATTGTCCATTCCTTGTGTGTCTTCTAC - 23460
    -FRGGLLTFTSKIVHSLCVFY
      S E V G C * L S Q A R L S I P C V S S T
       Q R W V V D F H K Q D C P F L V C L L L
23461 - TGCCAGAACTTCAAATGAATTTGAAGTATCTACTGGCTTTGTACTCCAAAGACAACGTAA - 23520
     -CQNFK*I*SIYWLCTPKTT*
    - ARTSNEFEVSTGFVLQRQRK
       PELQMNLKYLLALYSKDNVN
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23521 - ACACCAAGTGTTTGGATTGTCTTGGTTGTAGCCTGGTTAATGTGCCAAACAAT - 23580
    -TPSVWFERCLGCSLVNVPNN
    - H Q V F G L N V V L V V A W L M C Q T I
     TKCLV*TLSWL*PG*CAKQL
23581 - TGGCTTATGCAGTAATTTAGCACCTTTCTTGAAACTCGCTGAATAGTGTCTATAGTCAAT - 23640
    \hbox{-} \hbox{W L M Q * F S T F L E T R * I V S I V N}
    - G L C S N L A P F L K L A E * C L * S I
      A Y A V I * H L S * N S L N S V Y S Q *
23641 - AGCCACTACATCGCCATTCAAGTCTGGGAAGAATGTGACAGATAGCTCTCGTGAAGCTGG - 23700
    -SHYIAIQVWEECDR*LS*SW
    A T T S P F K S G K N V T D S S R E A G
      PLHRHSSLGRM * QIALVKLA
23701 - CTTTGTGAAGCCTGTCATTTGATTTAAATCATCAGCAAATTTTGTGTTAGAACATGTGAG - 23760
    -LCEACHLI*IISKFCVRTCE
     FVKPVI*FKSSANFVLEHVS
      L * S L S F D L N H Q Q I L C * N M * V
23761 - TTTGAAATTATCAAAACTCGCATTTGGTAATGGTTGAGTTGGTACAAGGTCTATAGGCTG - 23820
    -FEIIKTRIW * WLSWYKVYRL
     LKLSKLAFGNG * VGTRSIGC
     * N Y Q N S H L V M V E L V Q G L * A A
23821 - CTCTGTATAGTAAGCATTATCCTTTTTATAATACCCATCCAATTTTGGTTCAATCTCTGT - 23880
    -LCIVSIILFIIPIQFWFNLC
     SV * * A L S F L * Y P S N F G S I S V
      LYSKHYPFYNTHPILVQSLC
23881 - GTAAGTAACTCCATCGAGTTTATACGACACAGGCTTGATGGTTGTAGTGTAAGATGTTTC - 23940
    -VSNSIEFIRHRLDGCSVRCF
      K * L H R V Y T T Q A * W L * C K M F P
23941 - CTTGTAGAAAACATCAGTCACTGGTCCTTTGTACTCTGACATCTTTGTAAGGTGAGCTCC - 24000
    -LVENISHWSFVL*HLCKVSS
-L*KTSVTGPLYSDIFVR*AP
      CRKHQSLVLCTLTSL*GELR
24001 - GTCAATACGATAGAGGGTCTCCTTAGCAGTTATATGAGTGTAATGACCACACTGATAGTT - 24060
    -VNTIEGLLSSYMSVMTTLIV
    - S I R * R V S L A V I * V * * P H * * L
    - QYDRGSP*QLYECNDHTDSY
24061 - ACCAGTGTACTCATTCGCACATAAGAATGTACCTTGCTGTAATTTATACTCAGCAGGTGG - 24120
    -TSVLIRT*ECTLL*FILSRW
    - PVYSFAHKNVPCCNLYSAGG
      Q C T H S H I R M Y L A V I Y T Q Q V V
24121 - TGCAGACATCATAACAAAAGAAGACTCTTGTTGTACTAGATATTGTGTAGCATCACGACC - 24180
    -CRHHNKRRLLLY*ILCSITT
    - A D I I T K E D S C C T R Y C V A S R P
      Q T S * Q K K T L V V L D I V * H H D H
24181 - ACACACACATGGAATGGAAACACCTGTCTTAAGATTATCATAAGATAGAGTACCCATATA - 24240
    -THTWNGNTCLKIIIR * STHI
    - H T H G M E T P V L R L S * D R V P I Y
       T H M E W K H L S * D Y H K I E Y P Y T
24241 - CATCACAGCTTCTACACCCGTTAAGGTAGTTTTCTGACCACAATGTTTACACACCAC - 24300
    - H H S F Y T R * G S S F L T T M F T H H
      I T A S T P V K V V V F * P Q C L H T T
S Q L L H P L R * * F S D H N V Y T P H
24301 - ATTAAGAACTCGCTTTGCAGATTCCAAATTAGCATGCTGTAGAAGATGGGTCATAGTTTC - 24360
    -IKNSLCRFQISML * KMGHSF
    - L R T R F A D S K L A C C R R W V I V S
         E L A L Q I P N * H A V E D G S * F L
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24361 - TCTGACATCACCAAGCTCGCCAACAGTTTTATTACTGTAAGCGAGTATGAGTGCACAAAA - 24420
    -SDITKLANSFITVSEYECTK
    - L T S P S S P T V L L L * A S M S A Q K
      * H H Q A R Q Q F Y Y C K R V * V H K S
24421 - GTTAGCAGCATCACCAGCACGGGCTCTATAATAAGCCTCTTGAAGTGCTGGTGCATTGAA - 24480
    -VSSITSTGSIISLLKCWCIE
    - L A A S P A R A L * * A S * S A G A L N
      * Q H H Q H G L Y N K P L E V L V H * I
24481 - TTTGACTTCAAGCTGTTGAAGTGCTAATAAAACACTAGACAAATAACAATTGTTATCAGC - 24540
    -FDFKLLKC * * N T R Q I T I V I S
     LTSSC*SANKTLDK*QLLSA
       * L Q A V E V L I K H * T N N N C Y Q P
24541 - CCATTTAATTGAAGTTAAACCACCAACTTGAGGAAATTTCCATTTCTTTGTGTGGTTTAA - 24600
    - P F N * S * T T N L R K F P F L C V V *
     H L I E V K P P T * G N F H F F V W F K
      I * L K L N H Q L E E I S I S L C G L K
24601 - AGCAGACATGTACCTACCAAGAAAACTCTCATCAAGAGTATGGTAGTACTCGAAAGCTTC - 24660
    -SRHVPTKKTLIKSMVVLESF
     ADMYLPRKLSSRVW*YSKAS
      Q T C T Y Q E N S H Q E Y G S T R K L H
24661 - ACTACGTAGTGTCATCACTAGGTAGTACAAAGAAGTCTTACCCTCATGATTTACATG - 24720
    -TT * C V I T R * Y K E S L T L M I Y M
     LRSVSSLGSTKKVLPS*FT*
      Y V V C H H * V V Q R K S Y P H D L H E
24721 - AGGTTTAATTTTTGTAACATCAGCACCATCCAAGTATGTTGGACCAAACTGCTGTCCATA - 24780
    -R F N F C N I S T I Q V C W T K L L S I
     G L I F V T S A P S K Y V G P N C C P Y
      V * F L * H Q H H P S M L D Q T A V H M
24781 - TGTCATAGACATATCCACAAGCTGTGTGTGGAGATTAGTGTTGTCCACAGTTGTGAACAC - 24840
    -CHRHIHKLCVEISVVHSCEH
      V I D I S T S C V W R L V L S T V V N T
       S * T Y P Q A V C G D * C C P Q L * T L
24841 - TTTTATAGTCTTAACCTCCCGCAGGGATAAGAGACTCTTTAGTTTGTCAAGTGAAAGAAC - 24900
    - F Y S L N L P Q G * E T L * F V K * K N
- F I V L T S R R D K R L F S L S S E R T
     L * S * P P A G I R D S L V C Q V K E P
24901 - CTCACCGTCAAGATGAAACTCGACGGGGCTCTCCAGAGTGTGGTACACAATTTTGTCACC - 24960
    -LTVKMKLDGALQSVVHNFVT
    - S P S R * N S T G L S R V W Y T I L S P
     H R Q D E T R R G S P E C G T Q F C H H
24961 - ACGCTTAAGAAATTCAACACCTAACTCTGTACGCTGTCCTGAATAGGACCAATCTCTGTA - 25020
    -TLKKFNT*LCTLS*IGPISV
    - R L R N S T P N S V R C P E * D Q S L *
       A * E I Q H L T L Y A V L N R T N L C K
25021 - AGAGCCAGCCAAAGAAACTGTTTCTACAAAGTGCTCCTCAGATGTCTTTGATGACGAAGT - 25080
    -RASQRNCFYKVLLRCL**RS
      SQPKKLFLQSAPQMSLMTK*
25081 - GAGGTATCCATTATATGTAGTAACAGCATCTGGTGATGATACTGACACTACGGCAGGAGC - 25140
    -EVSIICSNSIW**Y*HYGRS
    - R Y P L Y V T A S G D D T D T T A G A
       G I H Y M * * Q H L V M I L T L R Q E L
25141 - TTTAAGAGAACGCATACAGCGCGCAGCCTCTTCAAGATTAAAACCATGTGTCACATAACC - 25200
    -FKRTHTARSLFKIKTMCHIT
     LRERIQRAASSRLKPCVT * P
         E N A Y S A Q P L Q D * N H V S H N Q
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25201 - AATTGGCATTGTGACAAGCGGCTCATTTAGAGAGTTCAGCTTCGTAATAATAGAAGCTAC - 25260
    -NWHCDKRLI*RVQLRNNRSY
    - I G I V T S G S F R E F S F V I I E A T
       L A L * Q A A H L E S S A S * * * K L Q
25261 - AGGCTCTTTACTAGTATAAAAGAAGAATCGGACACCATAGTCAACGATGCCCTCTTGAAT - 25320
    -RLFTSIKEESDTIVNDALLN
    - G S L L V * K K N R T P * S T M P S * I
       A L Y * Y K R R I G H H S Q R C P L E F
25321 - TTTAATTCCTTTATACTTACGTTGGATGGTTGCCATTATGGCTCTAACATCCATGCATAT - 25380
    - F N S F I L T L D G C H Y G S N I H A Y
      LIPLYLRWMVAIMALTSMHI
       * F L Y T Y V G W L P L W L * H P C I *
25381 - AGGCATTAATTTCTTGTCTCTCAGCATGAGCAAGCATTCTCTCAAATTCCAGGATAC - 25440
    -RH*FSCLFSMSKHFSQIPGY
      G I N F L V S S A * A S I S L K F Q D T
      A L I F L S L Q H E Q A F L S N S R I Q
25441 - AGTTCCTAGAATCTCTTCCTTAGCATTAGGTGCTTCTGAAGGTAGTACATAAAATGCAGA - 25500
    -SS*NLFLSIRCF*R*YIKCR
      V P R I S S L A L G A S E G S T * N A D
       F L E S L P * H * V L L K V V H K M Q I
25501 - TTTGCATTTCTTAAGAGCAGTCTTAGCTTCCTCAAGTGTATAACCAGCACATCCTTGTCC - 25560
    -FAFLKSSLSFLKCITSTSLS
    - L H F L R A V L A S S S V * P A H P C P
      CIS * E Q S * L P Q V Y N Q H I L V Q
25561 - AGGGTACGTGGTTATATACTCATCAACTGGCACTTTCTTCAAAGCTCTTGAGAGCATCTC - 25620
     -RVRGYILINWHFLQSS*EHL
      G Y V V I Y S S T G T F F K A L E S I S
    - GTWLYTHQLALSSKLLRASQ
25621 - AGTAGTGCCACCAGCCTTTTTGGAGGGTATTACAACACAAGTGATATCACCACTAGTGAT - 25680
     -SSATSLFGGYYNTSDITTSD
      V V P P A F L E G I T T Q V I S P L V I
       * C H Q P F W R V L Q H K * Y H H * * *
25681 - AACATCACCTACCATGTAAGGTGCATCCTTCTCAAGGAAAGACATATCTTCACCTCTAAG - 25740
     -NITYHVRCILKERHIFTSK
     - T S P T M * G A S F S R K D I S S P L S
      H H L P C K V H P S Q G K T Y L H L * A
25741 - CATGTTCTGAGAATCATGGTAAAGCTTACCATTGATATCAGCAAACAAGAGTAACTTATT - 25800
     -HVLRIMVKLTIDISKQE*LI
     - M F * E S W * S L P L I S A N K S N L L
       C S E N H G K A Y H * Y Q Q T R V T Y W
25801 - GGTAAGAAACTTAGTTTCTTCCAGTGTTGTGGTAACCTCATCAATGCAGGCCTTAATTTT - 25860
     -GKKLSFFQCCGNLINAGLNF
      V R N L V S S S V V V T S S M Q A L I F
      * E T * F L P V L W * P H Q C R P * F L
25861 - TGGCTTCACATCGACAGGCTTCTGTACGACAGATTTCTCCTCAGTTTTGGAATCTTCTGT - 25920
     -WLHIDRLLYDRFLLSFGIFC
-GFTSTGFCTTDFSSVLESSV
       A S H R Q A S V R Q I S P Q F W N L L C
 25921 - GTTTGGTGGCTCCTTGTTTAGGTGCTTCCACTCTAGGCTTCAGGTTATCAAGATAATC - 25980
     -V W W L L L F R C F H S R L Q V I K I I
      F G G S S C L G A S T L G F R L S R * S
       L V A P L V * V L P L * A S G Y Q D N P
 25981 - CATGACAACCTGCTCATAAAGAGCTTTGTCATTGACTGCAATATAAACCTGTGTACGAAC - 26040
     - H D N L L I K S F V I D C N I N L C T N
       M T T C S * R A L S L T A I * T C V R T
          Q P A H K E L C H * L Q Y K P V Y E P
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26041 - CGTCTGCACGCACACTTGTAAAGACTGAAGTGGTTTAGCACCAAATATGCCTGCTGACAA - 26100
    -RLHAHL*RLKWFSTKYAC*Q
    - V C T H T C K D * S G L A P N M P A D N
       S A R T L V K T E V V * H Q I C L L T T
26101 - CAATGGTGCAAGTAAGATGTCCTGTGAATTGAAATTTTCATATGCTGCCTTAAGAAGCTG - 26160
    -Q W C K * D V L * I E I F I C C L K K L
    - N G A S K M S C E L K F S Y A A L R S W
       M V Q V R C P V N * N F H M L P * E A G
26161 - GATGTCCTCACCTGCATTTAGGTTAGGTCCAACAACATGCAGACACTTCTTAGCAAGATT - 26220
    -DVLTCI*VRSNNMQTLLSKI
      M S S P A F R L G P T T C R H F L A R L
       C P H L H L G * V Q Q H A D T S * Q D Y
26221 - ATGTCCAGAAAGCAAACAAGACCCTCCTACTGTAAGAGGGCCATTTAGCTTAATGTAATC - 26280
    -MSRKQTRPSYCKRAI*LNVI
      C P E S K Q D P P T V R G P F S L M * S
       V Q K A N K T L L L * E G H L A * C N H
26281 - ATCACTCTCCTTTTGCATGGCACCATTGGTTGCCTTGTTGAGTGCACCTGCTACACCACC - 26340
    -I T L L H G T I G C L V E C T C Y T T
      S L S F C M A P L V A L L S A P A T P P
      HSPFAWHHWLPC*VHLLHHH
26341 - ACCATGTTTCAGGTGTATGTTAGCAGCATTTACAATCACCATAGGATTAGCACTTTGTGC - 26400
     -T M F Q V Y V S S I Y N H H R I S T L C
      P C F R C M L A A F T I T I G L A L C A
    - HVSGVC * QHLQSP * D * HFVP
26401 - CTCCTTAACGATGTCAACACATTTAATGGCAACATTGTCAGTAAGTTTTAAATAACCAGT - 26460
    -LLNDVNTFNGNIVSKF*ITS
    - S L T M S T H L M A T L S V S F K * P V
      P * R C Q H I * W Q H C Q * V L N N Q *
26461 - AAACTGATTAACTGGTTCTCAGGTGTAGGTTCTGGTTCTGGCTCAATCTCTGATTGCTC - 26520
     -KLINWFFRCRFWFWLNL*LL
     - N * L T G S S G V G S G S I S D C S
       \begin{smallmatrix} T&D&*&L&V&L&Q&V&*&V&L&V&L&A&Q&S&L&I&A&Q\\ \end{smallmatrix}
26521 - AGTAGTATCATCCAGCCAGTCTTCCTCTTCTTCTTCCTCAACTCGAACTGTTTCAGCTGA - 26580
     -SSIIQPVFLFFFLNSNCFS*
      V V S S S Q S S S S S S S T R T V S A E
       * Y H P A S L P L L L P Q L E L F Q L R
26581 - GGCACCAAATTCCAGAGGGAGACCTTGATAATCATCCTCTGTACCGTACTCATGTTCACA - 26640
     -G T K F Q R E T L I I L C T V L M F T
     - A P N S R G R P * * S S V P Y S C S Q
       H Q I P E G D L D N H P L Y R T H V H R
26641 - GGTTTCATCAATTTCTTCCTCACACTCTGCATCGTCCTCTTCTTCCTCATCTGGAGG - 26700
     -G F I N F F F L T L C I V L F F L I W R
       V S S I S S S S H S A S S S S S S G G
        F H Q F L L P H T L H R P L L P H L E G
26701 - GTAAAAGGAACAATACATACGTGATGAAAAGTTTTCTTCACCAGCATCATCAAATAAGTA - 26760
     -V K G T I H T * * K V F F T S I I K * V
        KEQYIRDEKFSSPASSNK*
        K R N N T Y V M K S F L H Q H H Q I S R
 26761 - GAATGTAGCTACACTCCACTCATCAAGATCAATACCCATGTTGGTAAGGAGATCAGAAAC - 26820
     -ECSYTPLIKINTHVGKEIRN
       N V A T L H S S R S I P M L V R R S E T
        M * L H S T H Q D Q Y P C W * G D Q K L
 26821 - TGGTTGTAAAGTCTTCACAACAGCCTCTGCTACAACACATGCAAACTCAGTAACTTCGGT - 26880
     -W L * S L H N S L C Y N T C K L S N F G
       G C K V F T T A S A T T H A N S V T S V
        V V K S S Q Q P L L Q H M Q T Q * L R Y
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26881 - ACCGGATTCAACAGTGTAGACAGAGCACTTTTCATTAAGCACTTTGTCAACACGTTCATC - 26940
    -TGFNSVDRALFIKHFVNTFI
    - P D S T V * T E H F S L S T L S T R S S
      RIQQCRQSTFH * ALCQHVHQ
26941 - AAGCTCAAATGTGATTCTCACATTCTTGTAACCTTGAACTTCCCAAACAGTATCTTCTCC - 27000
    - K L K C D S H I L V T L N F P N S I F S
    - S S N V I L T F L * P * T S Q T V S S P
      A Q M * F S H S C N L E L P K Q Y L L Q
- K G Y T F N W C T P F * A K D I V C S Q
     K V T P L I G A P P F K R K T L F V A S
      R L H L * L V H P L L S E R H C L * P V
27061 - TAAACCAGGAGACAATGCGCAGTATTGTTCTTTGTCCTTAATCTCTAAGAGCATGAGGCC - 27120
    - * T R R Q C A V L F F V L N L * E H E A
    - K P G D N A Q Y C S L S L I S K S M R P
      NQETMRSIVLCP*SLRA*GH
27121 - ATTTACACAGACTGGTGTGCCGACGATAGCTCCATTTGTGAAGCTATCAACGGGCGTCTC - 27180
    -IYTDWCADDSSICEAINGRL
     F T Q T G V P T I A P F V K L S T G V S
      L H R L V C R R * L H L * S Y Q R A S R
27181 - GAGTGCTTCGAGTTCACCGTTCTTGAGAACAACCTCCTCAGAGGTAAGTACTGTGTCATG - 27240
    -ECFEFTVLENNLLRGKYCVM
     S A S S P F L R T T S S E V S T V S C
      V L R V H R S * E Q P P Q R * V L C H V
27241 - TGAATCACCTTCAAGAAAGGTTACTTCTTTTGGTGCCTTAAGAGGCATGAGTAGTTGCAG - 27300
    -*ITFKKGYFFWCLKRHE*LQ
     ESPSRKVTSFGALRGMSSCS
      N H L Q E R L L L V P * E A * V V A A
27301 - CTGCTCCTTGCCACGTATACACTGACGGTAAAGTCCCTTGCTTTGAGCGATGAAGACTTC - 27360
    -LLLATYTLTVKSLALSDEDF
    - C S L P R I H * R * S P L L * A M K T S
      APCHVYTDGKVPCFER*RLH
27361 - ACCTAAGTTGAGTGATCGCAACTTTGCGCCAGCGATAGTGACTTGATCAATGCACATTTC - 27420
    T * V E * S Q L C A S D S D L I N A H F
    - PKLSDRNFAPAIVT*SMHIS
      LS * VIATLRQR * * LDQCTFR
27421 - GAGTGCCTTGTTAACAACATCAATGAAGCATTTTACACAATCCTTGATGTTATCTGAAGC - 27480
    -ECLVNN EAFYTILDVI*S
    - S A L L T T S M K H F T Q S L M L S E A
       V P C * Q H Q * S I L H N P * C Y L K Q
27481 - AACCTGTATTTGACCCTTGACGATGTCAAAAACACCTGTAATGAGAAATTTGAGAATCTC - 27540
    -NLYLTLDDVKNTCNEKFENL
      TCI*PLTMSKTPVMRNLRIS
       PVFDP*RCQKHL**EI*ESP
27541 - CCAAGCATCCTTGAGAAATTCAACTCCTGCACTAAGTTTCGCCTCAATCCATTCAAAGAT - 27600
    - P S I L E K F N S C T K F R L N P F K D
      Q A S L R N S T P A L S F A S I H S K I
       K H P * E I Q L L H * V S P Q S I Q R *
27601 - AGGCCTGAGTTTTCAACAGTAGTGCCCAAAAGATTAGACAACCACTGAGAAGTCTGTTG - 27660
     -RPEFFNSSAQKIRQPLRSLL
      G L S F S T V V P K R L D N H * E V C C
      A * V F Q Q * C P K D * T T T E K S V V
27661 - TACAAGACCACCAGTTACATATGCCATAATAATGACACTGTTGGTGAGCAGGTCTGAAGT - 27720
    -Y K T T S Y I C H N N D T V G E Q V * S
      TRPPVTYAIIMTLLVSRSEV
        D H Q L H M P * * * H C W * A G L K Y
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27721 - ATAAACCATGGCGTCGACAAGACGTAATGACTGTTCAGAAATACCATCAAGTATGGTGAC - 27780
    -INHGVDKT**LFRNTIKYGD
    - * T M A S T R R N D C S E I P S S M V T
      K P W R R Q D V M T V Q K Y H Q V W * Q
27781 - AGCTGCTCTTTGCAAATCAGGAATTGAGTGGTTTGCTGCATCAAGTGTGCGCGCAAAAAT - 27840
    -SCSLQIRN*VVCCIKCARKN
    - A A L C K S G I E W F A A S S V R A K I
      L L F A N Q E L S G L L H Q V C A Q K L
27841 - TGATCTGATAACACCAGCAGCCTGTGAGGGAAAACCACACAGTGGTGTTAAAACTGATCT - 27900
    - * S D N T S S L * G K T T Q W C * N * S
     D L I T P A A C E G K P H S G V K T D L
      I * * H Q Q P V R E N H T V V L K L I S
27901 - CTGTTGTCCAATGTTCCAAGCACCTTTTACGGGCTTTCCCTTGGTAACTTTATAGTTACC - 27960
    -LLSNVPSTFYGLSLGNFIVT
     C C P M F Q A P F T G F P L V T L * L P
      V V Q C S K H L L R A F P W * L Y S Y R
27961 - GCAGGACTCAACAATGGTTTTGAAAGACTTGTAATCAAGACTCTTTATAGTGTCAATAAA - 28020
    - A G L N N G F E R L V I K T L Y S V N K
      Q D S T M V L K D L * S R L F I V S I K
      RTQQWF*KTCNQDSL*CQ*R
-GTCRSRERCQNDGNLFIQMK
     A L V E A E K D A K M M A T S S F K * K
    - H L * K Q R K M P K * W Q P L H S N E N
28081 - ATCGCCAACAATGTTAATGTTAACACGTTCACGACTCAGTATCTCAAGGAGATCCTCATT - 28140
    - I A N N V N V N T F T T Q Y L K E I L I
      SPTMLMLTRSRLSISRRSSF
      R Q Q C * C * H V H D S V S Q G D P H S
28141 - CAAGGTCTCCACATTGTCACCAGTAATGCCAGTATGGCCTGAGCCAATATCAGCACTAGC - 28200
    -QGLHIVTSNASMA*ANISTS
    - K V S T L S P V M P V W P E P I S A L A
     R S P H C H Q * C Q Y G L S Q Y Q H * H
-TRNPVGTLIIAANIGKHTAS
    - R G T Q * A R L L * Q P T * A N T Q P P
       E E P S R H A Y Y S S Q H R Q T H S L Q
28261 - AAAACATCTAGTCCTACCTCCCTTGCGGAGTCGAGTTTCAATGTTTGAGTGGTTGTGATA - 28320
    -KTSSPTSLAESSFNV*VVI
    - K H L V L P P L R S R V S M F E W L * *
      N I * S Y L P C G V E F Q C L S G C D N
- I C N T M L R S N L W V L T G R T W H F
- S A T L C S G P I S G S * Q A G H G I F
       L Q H Y A Q V Q S L G L D R Q D M A F S
28381 - CACTACAGCATTAGTAGGTACCCACATGTAGTAGGTCCTTCAATAACTAAATTTTC - 28440
    - H Y S I S R * V P T C S R S F N N * I F
     T T A L V G R Y P H V V G P S I T K F S
L Q H * * V G T H M * * V L Q * L N F Q
28441 - AGTGCCACAATGTTCACAAGTGGCTTTCAGAAAGTCGCACGTCTGCCATGAAACTTCATC - 28500
    -SATMFTSGFQKVARLP*NFI
     . V P Q C S Q V A F R K S H V C H E T S S
       C H N V H K W L S E S R T S A M K L H R
28501 - GCAATGATTACATTTCATCAAGGTAGACAAGTGCATATTGTTACACTCCTGTGGAGATGC - 28560
    - A M I T F H Q G R Q V H I V T L L W R C
    - Q * L H F I K V D K C I L L H S C G D A
       N D Y I S S R * T S A Y C Y T P V E M Q
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28561 - AACAGGGTACACAGAGCGTATACGCCCCATGAAACCCTCAGTCTTTTCTTTTCAACACG - 28620
   -NRVHRAYTPHETLSLFNT
   - T G Y T E R I R P M K P S V F F S T R
      Q G T Q S V Y A P * N P Q S F S F Q H V
28621 - TGGTTGAATGACTTTGACTTTTGAGTTAAGAGGAAACACAAACTTTGGGCATTCCCCTTT - 28680
   -WLNDFDF*VKRKHKLWAFPF
    - G * M T L T F E L R G N T N F G H S P L
      VE*L*LLS*EETQTLGIPL*
28681 - GAAAGTGTCAAATTTCTTGGCACTCTTAATTTCGAAGGGTGTCTGGTGCTCGTAGCTCTT - 28740
    -ESVKFLGTLNFEGCLVLVAL
    KVSNFLALLISKGVWCS*LL
      KCQISWHS*FRVSGARSSY
28741 - ATCAGAGCGCTCAGTGAACCAGGCAATTTCATGCTCATGGTCACGGCAGCAGTAGACACC - 28800
    - I R A L S E P G N F M L M V T A A V D T
     SERSVNQAISCSWSRQQ*TP
      Q S A Q * T R Q F H A H G H G S S R H L
28801 - TCTCTTCGACTCGATGTAATCAAGTTGTTCGGAAAGAGTGCACATTGACTTGCCCGCGCG - 28860
    -SLRLDVIKLFGKSAH * LARA
     L F D S M * S S C S E R V H I D L P A R
     S S T R C N Q V V R K E C T L T C P R V
28861 - TGCGAGAAAATCTTTGATGCAATCAAGAGGGTACCCATCTGGGCCACAGAAATTGTTGTC - 28920
    -CEKIFDAIKRVPIWATEIVV
     ARKSLMQSRGYPSGPQKLLS
     RENL * CNQEGTHLGHRNCCR
-DIASDCTSIELTSEFTECTT
     T * R V T A P P L S S R V S S R S A P L
      HSE*LHLH*AHE*VHGVHHC
28981 - GCCATGCTTAGTGTTCCAGTTTTGTTCATAATCTTCAATGGGATCAGTGCCAAGCTCGTC - 29040
    -AMLSVPVLFIIFNGISAKLV
-PCLVFQFCS*SSMGSVPSS
     HA*CSSFVHNLQWDQCQARH
29041 - ACCTAAGTCATAAGACTTTAGATCGATGCCATAGCTATGACCACCGGCTCCCTTATTACC - 29100
    -T * V I R L * I D A I A M T T G S L I T
     P K S * D F R S M P * L * P P A P L L P
      L S H K T L D R C H S Y D H R L P Y Y R
29101 - GTTCTTACGAAGAACATTGCGGTATGCAATTGGGGTTTCGCCCACATGTGGCACGAG - 29160
    -VLTKKNIAVCNWGFAHMWHE
      F L R R R T L R Y A I G V S P T C G T S
      S Y E E E H C G M Q L G F R P H V A R V
29161 - TACTCCCAGTGTTATACCGCTACGACCGTACTGAATGCCGTCCATTTCTGCAACCAGCTC - 29220
    - Y S Q C Y T A T T V L N A V H F C N Q L
      T P S V I P L R P Y * M P S I S A T S S
      L P V L Y R Y D R T E C R P F L Q P A Q
29221 - AACGACCTTGTGGCCGTGATTGGTGCTTAAGGCATCAGAACGTTTAATGAACACATAGGG - 29280
    -NDLVAVIGA*GIRTFNEHIG
      TTLWP*LVLKASERLMNT*G
      R P C G R D W C L R H Q N V * * T H R A
29281 - CTGTTCAAGCTGGGGCAGTACGCCTTTTTCCAGCTCTACTAGACCACAAGTGCCATTTTT - 29340
    -LFKLGQYAFFQLY*TTSAIF
     C S S W G S T P F S S S T R P Q V P F L
      V Q A G A V R L F P A L L D H K C H F *
29341 - GAGGTGTTCACGTGCCTCCGATAGGGCCTCTTCCACAGAGTCCCCGAAGCCACGCACTAG - 29400
    -EVFTCLR * GLFHRVPEATH *
    - R C S R A S D R A S S T E S P K P R T S
      G V H V P P I G P L P Q S P R S H A L A
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90/90

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29401 - CACGTCTCTAACCTGAAGGACAGGCAAACTGAGTTGGACGTGTGTTTTCTCGTTGACACC - 29460
    - H V S N L K D R Q T E L D V C F L V D T
    - T S L T * R T G K L S W T C V F S L T P
    - RL * PEGQAN * VGRVFSR * HQ
29461 - AAGAACAAGGCTCTCCATCTTACCTTTCGGTCACACCCGGACGAAACCTAGGTATGCTGA - 29520
    -KNKALHLTFRSHPDET * VC *
    - R T R L S I L P F G H T R T K P R Y A D
    - EQGSPSYLSVTPGRNLGMLM
29521 - TGATCGACTGCAACACGGACGAAACCGTAAGCAGTCTGCAGAAGAGGGGACGAGTTACTCG - 29580
    - * S T A T R T K P * A V C R R G T S Y S
    - D R L Q H G R N R K Q S A E E G R V T R
     I D C N T D E T V S S L Q K R D E L L V
29581 - TTTCTTGTCAACGACAGTAAAATTTATTATTGTTTATACTGCGTAGGTGCACTAGGCATG - 29640
    -FLVNDSKIYYCLYCVGALGM
    - F L S T T V K F I I V Y T A * V H * A C
     SCQRQ*NLLLFILRRCTRHA
29641 - CAGCCGAGCGACAGCTACACAGATTTTAAAGTTCGTTTAGAGAACAGATCTACAAGAGAT - 29700
    -QPSDSYTDFKVRLENRSTRD
    - S R A T A T Q I L K F V * R T D L Q E I
     AERQLHRF*SSFREQIYKRS
29701 - CGAGGTTGGTTGGCTTTTCCTGGGTAGGTAAAAACCTAATAT - 29742
    -RGWLAFPG*VKT*YX
    - E V G W L F L G R * K P N X
     RLVGFSWVGKNLIX
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FIG. 12 Con't